



# STIC Search Report

## Biotech-Chem Library

STIC Database Tracking Number: 160995

TO: Ruixiang Li  
Location: REM/4D75/4C70  
Art Unit: 1646  
Monday, August 08, 2005

Case Serial Number: 10/626126

From: Edward Hart  
Location: Biotech-Chem Library  
REM-1A55  
Phone: 571-272-2512

[edward.hart@uspto.gov](mailto:edward.hart@uspto.gov)

### Search Notes

Examiner Li,

Here are the results of the search you requested.

Please feel free to contact me if you have any questions.

Edward Hart

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STIC-Biotech/ChemLib

168995

From: Li, Ruixiang  
Sent: Friday, July 29, 2005 4:06 PM  
To: STIC-Biotech/ChemLib  
Subject: Sequence search of Application No.10/626,126

Please do a standard search on:

- (i). SEQ ID NO: 9 against commercial amino acid databases.
- (ii). SEQ ID NOS: 6 and 9 against commercial nucleic acid databases.

Thank you very much!

Ruixiang Li  
GAU 1646  
REM 4D75  
Mail Box 4C70  
(571) 272-0875

RECEIVED  
JUL 29 2005  
STIC-Biotech Division

\*\*\*\*\*

STAFF USE ONLY

Searcher: \_\_\_\_\_  
Searcher Phone: 2- \_\_\_\_\_  
Date Searcher Picked up: 8/1/05  
Date Completed: \_\_\_\_\_  
Searcher Prep/Rev. Time: \_\_\_\_\_  
Online Time: \_\_\_\_\_

\*\*\*\*\*

Type of Search

NA#: 1 AA#: 171 reverse to NA  
Interference: \_\_\_\_\_ SPDI: \_\_\_\_\_  
S/L: \_\_\_\_\_ Oligomer: \_\_\_\_\_  
Encode/Transl: \_\_\_\_\_  
Structure#: \_\_\_\_\_ Text: \_\_\_\_\_  
Inventor: \_\_\_\_\_ Litigation: \_\_\_\_\_

\*\*\*\*\*

Vendors and cost where applicable

STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
QUESTEL/ORBIT: \_\_\_\_\_  
LEXIS/NEXIS: \_\_\_\_\_  
SEQUENCE SYSTEM: OSp  
WWW/Internet: \_\_\_\_\_  
Other(Specify): \_\_\_\_\_

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 5, 2005, 10:32:28 ; Search time 777 Seconds  
(without alignments)  
9811.087 Million cell updates/sec

Title: US-10-626-126-6  
Perfect score: 1176  
Sequence: 1 atgtcggagcttaacggcac.....cccgagtcagtattcttttga 1176

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 7297361 seqs, 3241162794 residues

Total number of hits satisfying chosen parameters: 14594722

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications NA:  
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25: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq.\*  
26: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1176	100.0	1176	20	US-10-626-445-6
2	1176	100.0	1176	21	US-10-626-126-6
3	1176	100.0	1176	20	US-10-626-398-6
4	958.4	81.5	1176	20	US-10-626-445-5
5	958.4	81.5	1176	21	US-10-626-126-5
6	958.4	81.5	1176	21	US-10-626-398-5
7	669	56.9	1173	9	US-09-812-216-1

669	56.9	1173	9	US-09-910-411-1	Sequence 1, Appli
669	56.9	1173	10	US-09-875-076-13	Sequence 13, Appl
669	56.9	1173	10	US-09-876-252-13	Sequence 13, Appl
669	56.9	1173	13	US-10-052-193-1	Sequence 1, Appli
669	56.9	1173	13	US-10-052-193-1	Sequence 26, Appl
669	56.9	1173	15	US-10-290-078-26	Sequence 13, Appl
669	56.9	1173	15	US-10-272-983-13	Sequence 1, Appli
669	56.9	1173	15	US-10-354-769-1	Sequence 13, Appl
669	56.9	1173	16	US-10-393-807-13	Sequence 13, Appl
669	56.9	1173	17	US-10-417-820A-13	Sequence 13, Appl
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669	56.9	1173	19	US-10-782-596-13	Sequence 13, Appl
669	56.9	1173	19	US-10-737-619-1	Sequence 1, Appli
669	56.9	1173	20	US-10-626-445-1	Sequence 1, Appli
669	56.9	1173	21	US-10-616-088-1	Sequence 1, Appli
669	56.9	1173	21	US-10-626-126-1	Sequence 1, Appli
669	56.9	1173	21	US-10-626-398-1	Sequence 1, Appli
669	56.9	1265	15	US-10-290-078-25	Sequence 25, Appl
669	56.9	1266	10	US-09-891-138A-5	Sequence 5, Appli
669	56.9	1300	10	US-09-852-165-1	Sequence 1, Appli
669	56.9	1300	19	US-10-696-673-1	Sequence 1, Appli
669	56.9	3689	15	US-10-225-567A-628	Sequence 628, App
669	56.9	3689	21	US-10-684-206-19	Sequence 19, Appl
616.8	52.4	1170	20	US-10-626-445-7	Sequence 7, Appli
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268.4	22.8	1326	19	US-10-398-036-19	Sequence 19, Appl
135	1239	9	9	US-09-891-053-2	Sequence 2, Appli
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158.4	13.5	2700	9	US-09-891-053-5	Sequence 5, Appli
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138.4	11.8	1335	9	US-09-350-206-3	Sequence 3, Appli
138.4	11.8	1335	9	US-09-349-755-3	Sequence 3, Appli
138.4	11.8	1335	9	US-09-166-334-3	Sequence 3, Appli
138.4	11.8	1335	15	US-10-282-958-3	Sequence 3, Appli
138.4	11.8	1335	19	US-10-727-021-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1  
US-10-626-445-6  
; Sequence 6, Application US/10626445  
; Publication No. US20040248252A1  
; GENERAL INFORMATION:  
; APPLICANT: Lovenberg, Timothy  
; APPLICANT: Liu, Changlu  
; TITLE OF INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Subtype  
; FILE REFERENCE: PRD-0032  
; CURRENT APPLICATION NUMBER: US/10/626,445  
; CURRENT FILING DATE: 2003-07-23  
; PRIOR APPLICATION NUMBER: 09/790,849  
; PRIOR FILING DATE: 2001-02-22  
; PRIOR APPLICATION NUMBER: 60/208,260  
; PRIOR FILING DATE: 2000-05-31  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 6  
; LENGTH: 1176  
; TYPE: DNA  
; ORGANISM: Rattus rattus  
US-10-626-445-6

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Db	1	ATGTCGGAGTCTAACGGCACTGACGTCTTGCCACTGCTCAAGTCCCTTGGCATTT	60	

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Db 61 TTAATGTCCTGCTGCTTTTGGCTATAAAGATAGGCAATGCTGTGTCAATTTTAGCCCTTT 120

QY 121 GTAGCAGACAGAAACCTTAGACATCGAAGTAATTAATTTTCTTAATTTGGCTATTCT 180
Db 121 GTAGCAGACAGAAACCTTAGACATCGAAGTAATTAATTTTCTTAATTTGGCTATTCT 180

QY 181 GACTTCTTCGTGGGTGTCATCTCCATTCCTCTGTACATCCCTCACACGCTGTTAACTGG 240
Db 181 GACTTCTTCGTGGGTGTCATCTCCATTCCTCTGTACATCCCTCACACGCTGTTAACTGG 240

QY 241 AATTTTGGAAAGTGAATCTGCATGTTTTGGCTCAATTAAGTACTGATCTTTTGTGCAGCA 300
Db 241 AATTTTGGAAAGTGAATCTGCATGTTTTGGCTCAATTAAGTACTGATCTTTTGTGCAGCA 300

QY 301 TCCGTCTACAGTATTTGTCCTCATTAGCTAGCATCGATACGATCCAGTCAGTTCCTCAACGCTGTG 360
Db 301 TCCGTCTACAGTATTTGTCCTCATTAGCTAGCATCGATACGATCCAGTCAGTTCCTCAACGCTGTG 360

QY 361 CGTTATAGACACAGCACACTGGCATCTGGAATTTGTTGCTCAAAATGTTGCTCAAAATGTTG 420
Db 361 CGTTATAGACACAGCACACTGGCATCTGGAATTTGTTGCTCAAAATGTTGCTCAAAATGTTG 420

QY 421 ATACTGGCTTTCTTGTGTCATGCCCCCAATGATTTCTGGCTTCGGATTTCTTGGAGAACAGC 480
Db 421 ATACTGGCTTTCTTGTGTCATGCCCCCAATGATTTCTGGCTTCGGATTTCTTGGAGAACAGC 480

QY 481 ACCAAACACAGAGGAGTCGGAGCTGGCTTTGTTACTGAGTGGTACATCTCCGCAATTACA 540
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QY 541 GCATTTCTTGGAAATTCCTGCTCCCTGTCTCCTTGGTGTCTATTTCAAGTGTACAGATTTAC 600
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QY 601 TGGAGCTGTGGAGCGTGGAGTCTCAGTAGGTGCCCTAGCCACGCTGGATTCATCGCT 660
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Db 661 ACCTCTTCCAGGGGCACTGGACACTCAGCAGAACTGGGTGGCTGTAGACAAAGTCTT 720

QY 721 CTTGGATTTAAAGGAACAGCGCGATCCCTTCATTACAGAAAGTCCACAGGAAAGAGAGT 780
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QY 781 CTCTGTGTCTTAAAGGACTCACATGAGCGGTAGTATCATCGCTTTCAAAGTGGGTTC 840
Db 781 CTCTGTGTCTTAAAGGACTCACATGAGCGGTAGTATCATCGCTTTCAAAGTGGGTTC 840

QY 841 TTCTGCGATCAGAAAGCCAGTGTCTTCCACAGAGAGACAGTGGAGCTTCTCAGAGGC 900
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QY 961 TATTGCTGTTCACAAATTTGTTCTTCACTTATCGCAGAGGGAGCGCCCAATCGATT 1020
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QY 1141 CCAGCACCTTTCAGACACCCAGTCAGTATCTTTCTTGA 1176
Db 1141 CCAGCACCTTTCAGACACCCAGTCAGTATCTTTCTTGA 1176
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## RESULT 2

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US-10-626-126-6
; Sequence 6, Application US/10626126
; Publication No. US20050074770A1
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Liu, Changlu
; TITLE OF INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Subtype
; FILE REFERENCE: PRD-0033
; CURRENT APPLICATION NUMBER: US/10/626,126
; CURRENT FILING DATE: 2003-07-23
; PRIOR APPLICATION NUMBER: 09/790,849
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/208,260
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 1176
; TYPE: DNA
; ORGANISM: Rattus rattus
US-10-626-126-6
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Query Match 100.0%; Score 1176; DB 21; Length 1176;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1176; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 61 TTAATGTCCTGCTGCTTTTGTATAAAGATAGGCAATGCTGTGTCAATTTAGCCCTTT 120
Db 61 TTAATGTCCTGCTGCTTTTGTATAAAGATAGGCAATGCTGTGTCAATTTAGCCCTTT 120

QY 121 GTAGCAGACAGAAACCTTAGACATCGAAGTAATTAATTTTCTTAATTTGGCTATTCT 180
Db 121 GTAGCAGACAGAAACCTTAGACATCGAAGTAATTAATTTTCTTAATTTGGCTATTCT 180

QY 181 GACTTCTTCGTGGGTGTCATCTCCATTCCTCTGTACATCCCTCACACGCTGTTAACTGG 240
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QY 241 AATTTTGGAAAGTGAATCTGCATGTTTTGGCTCAATTAAGTACTGATCTTTTGTGCAGCA 300
Db 241 AATTTTGGAAAGTGAATCTGCATGTTTTGGCTCAATTAAGTACTGATCTTTTGTGCAGCA 300

QY 301 TCCGTCTACAGTATTTGTCCTCATTAGCTAGCATCGATACGATCCAGTCAGTTCCTCAACGCTGTG 360
Db 301 TCCGTCTACAGTATTTGTCCTCATTAGCTAGCATCGATACGATCCAGTCAGTTCCTCAACGCTGTG 360

QY 361 CGTTATAGACACAGCACACTGGCATCTGGAATTTGTTGCTCAAAATGTTGCTCAAAATGTTG 420
Db 361 CGTTATAGACACAGCACACTGGCATCTGGAATTTGTTGCTCAAAATGTTGCTCAAAATGTTG 420

QY 421 ATACTGGCTTTCTTGTGTCATGCCCCCAATGATTTCTGGCTTCGGATTTCTTGGAGAACAGC 480
Db 421 ATACTGGCTTTCTTGTGTCATGCCCCCAATGATTTCTGGCTTCGGATTTCTTGGAGAACAGC 480

QY 481 ACCAAACACAGAGGAGTCGGAGCTGGCTTTGTTACTGAGTGGTACATCTCCGCAATTACA 540
Db 481 ACCAAACACAGAGGAGTCGGAGCTGGCTTTGTTACTGAGTGGTACATCTCCGCAATTACA 540

QY 541 GCATTTCTTGGAAATTCCTGCTCCCTGTCTCCTTGGTGTCTATTTCAAGTGTACAGATTTAC 600
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Qy	721	CCTGGATTAAAGGAACAGACCGCGATCCCTTCATTAGAAAGTCCACGAGGAAAGAGCAGT	780
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Qy	781	CTCTGGTGTCTTAAAGGACTCAGATGAGCGGTAGTATCATCGCCTTCAAAGTGGGTTC	840
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RESULT 3  
US-10-626-398-6  
; Sequence 6, Application US/10626398  
; Publication No. US20050074841A1  
; GENERAL INFORMATION:  
; APPLICANT: Lovenberg, Timothy  
; APPLICANT: Liu, Changlu  
; TITLE OF INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Subtype  
; FILE REFERENCE: PRD-0034  
; CURRENT APPLICATION NUMBER: US/10/626,398  
; CURRENT FILING DATE: 2003-07-23  
; PRIOR APPLICATION NUMBER: 09/790,849  
; PRIOR FILING DATE: 2001-02-22  
; PRIOR APPLICATION NUMBER: 60/208,260  
; PRIOR FILING DATE: 2000-05-31  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: Patent in version 3.2  
; SEQ ID NO 6  
; LENGTH: 1176  
; TYPE: DNA  
; ORGANISM: Rattus rattus  
US-10-626-398-6

Query Match	100.0%	Score 1176;	DB 21;	Length 1176;
Best Local Similarity	100.0%	Pred. No. 0;		
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Db	1	ATGTCGGAGTCTAACGGCACTGACGCTCTTGCCACTGACTGTCTCAAGTCCCTTGGCAATT	60	
Qy	61	TTAATGCTCCCTGCTGCTTTGCTATACGATAGGCAATGCTGTGGTCAATTTAGCCTTT	120	

Db	61	TTAATGCTCCCTGCTGCTTTTGTCTATAACGATAGGCAATGCTGTGGTCAATTTTAGCCTTT	120
Qy	121	GTAGCAGACAGAAACCTTAGACATCGAAGTAATATTTTTTCTTAATTTGGCTATTTCT	180
Db	121	GTAGCAGACAGAAACCTTAGACATCGAAGTAATATTTTTTCTTAATTTGGCTATTTCT	180
Qy	181	GACTTCTTGTGGGTGTCACTCCATTCTCTGTGTACATCCCTCACAGCTGTTTAACTGG	240
Db	181	GACTTCTTGTGGGTGTCACTCCATTCTCTGTGTACATCCCTCACAGCTGTTTAACTGG	240
Qy	241	AATTTTGAAGTGAATCTGTCATGTTTGGCTCAATTAAGTACTGACTATCTTTTGTGACAGCA	300
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Qy	301	TCCGTCTACAGTATTGTCCTCATTAAGTACGATACGATACGATCAGTTTCAAAAGCTGTG	360
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Qy	361	CGTTTATAGACACAGCACCTGGCATCTGGAATTTGCTCAAAATGGTGGCTGTTTGG	420
Db	361	CGTTTATAGACACAGCACCTGGCATCTGGAATTTGCTCAAAATGGTGGCTGTTTGG	420
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Db	421	ATACTGGCTTCTTGGTCAATGGCCCAATGATTCTGGCTTCGGATTCTTGAAGAAACAGC	480
Qy	481	ACCAACACAGAGGAGTGGGCTTTGTTTACTGAGTGGTATACCTCGCCATTACA	540
Db	481	ACCAACACAGAGGAGTGGGCTTTGTTTACTGAGTGGTATACCTCGCCATTACA	540
Qy	541	GCATTCTTGGNAATTCCTGCTCCCTGCTCTCTGGTGGTCTATTTTCAAGTGTACAGATTTAC	600
Db	541	GCATTCTTGGNAATTCCTGCTCCCTGCTCTCTGGTGGTCTATTTTCAAGTGTACAGATTTAC	600
Qy	601	TGGAGCTGTGGAGAGCTGGGAGTCTCAGTAGGTGCTTAGCCAGCGCTGGATTTCATCGCT	660
Db	601	TGGAGCTGTGGAGAGCTGGGAGTCTCAGTAGGTGCTTAGCCAGCGCTGGATTTCATCGCT	660
Qy	661	ACCTCTTCCAGGGGCACTGGACACTCAGCAGAACTGGGTTGGCTTGTAGACAAAGTCTT	720
Db	661	ACCTCTTCCAGGGGCACTGGACACTCAGCAGAACTGGGTTGGCTTGTAGACAAAGTCTT	720
Qy	721	CCTGGATTAAAGGAACAGCGCGATCCCTTCATTAGAAAGTCCACGAGGAAAGAGCAGT	780
Db	721	CCTGGATTAAAGGAACAGCGCGATCCCTTCATTAGAAAGTCCACGAGGAAAGAGCAGT	780
Qy	781	CTCTGCTGTCTTAAAGGACTCAGATGAGCGGTAGTATCATCGCCTTCAAAGTGGGTTC	840
Db	781	CTCTGCTGTCTTAAAGGACTCAGATGAGCGGTAGTATCATCGCCTTCAAAGTGGGTTC	840
Qy	841	TTCTGCCGATCAGAAAGCCAGTGTCTTCCAGAGAGAGACGCTGGAGCTTCTCAGAGGC	900
Db	841	TTCTGCCGATCAGAAAGCCAGTGTCTTCCAGAGAGAGACGCTGGAGCTTCTCAGAGGC	900
Qy	901	AGGAAGCTAGCCAGGTGCTAGCTGCTCTCTGAGTGTCTTTGGCATTTGCTGGGCTCCG	960
Db	901	AGGAAGCTAGCCAGGTGCTAGCTGCTCTCTGAGTGTCTTTGGCATTTGCTGGGCTCCG	960
Qy	961	TATTGCTGTTTCAAAATTTCTTTCAACTTATCGCAGAGGAGCGCCCAAAATCGATT	1020
Db	961	TATTGCTGTTTCAAAATTTCTTTCAACTTATCGCAGAGGAGCGCCCAAAATCGATT	1020
Qy	1021	TGGTACAGCAGTGTCTTGGCTACAGTGGTTCATTAATTAATCCCTTTCTATAC	1080
Db	1021	TGGTACAGCAGTGTCTTGGCTACAGTGGTTCATTAATTAATCCCTTTCTATAC	1080
Qy	1081	CCTTTGTGCCACAGAGCTTCCAGAGGCTTCTGGAAGATACCTGTGTGACAAAGCAA	1140
Db	1081	CCTTTGTGCCACAGAGCTTCCAGAGGCTTCTGGAAGATACCTGTGTGACAAAGCAA	1140
Qy	1141	CCAGACCTTCCAGAGCCAGTCAAGTATCTTCTTGA	1176
Db	1141	CCAGACCTTCCAGAGCCAGTCAAGTATCTTCTTGA	1176

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RESULT 4
US-10-626-445-5
; Sequence 5, Application US/10626445
; Publication No. US20040248252A1
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Liu, Changlu
; TITLE OF INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Subtype
; FILE REFERENCE: PRD-0032
; CURRENT APPLICATION NUMBER: US/10/626,445
; PRIOR FILING DATE: 2003-07-23
; PRIOR APPLICATION NUMBER: 09/790,849
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/208,260
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 1176
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-626-445-5

Query Match      81.5%; Score 958.4; DB 20; Length 1176;
Best Local Similarity 88.4%; Pred. No. 5e-295;
Matches 1040; Conservative 0; Mismatches 136; Indels 0; Gaps 0;

Qy 1 ATGTCGGAGTCTAACGGCACTGAGCTCTGCGCACTGCTGCAAGTCCCTTGGCATTT 60
Db 1 ATGTCGGAGTCTAACGGCACTGAGCTCTGCGCACTGCTGCAAGTCCCTTGGCATTT 60
Qy 61 TTAATGTCCTTGGTCTTGGTCTTGGTCTTGGTCTTGGTCTTGGTCTTGGTCTTGG 120
Db 61 TTAATGTCCTTGGTCTTGGTCTTGGTCTTGGTCTTGGTCTTGGTCTTGGTCTTGG 120
Qy 121 GTAGCAGACAGAAACCTTAGACATCGAAGTAATTTATTTTCTTAATTTGGCTATTCT 180
Db 121 GTAGCAGACAGAAACCTTAGACATCGAAGTAATTTATTTTCTTAATTTGGCTATTCT 180
Qy 181 GACTTCTTCGTGGGTGTCTCATTCCTCTGTACATCCCTCAGACGCTGTTTAACTGG 240
Db 181 GACTTCTTCGTGGGTGTCTCATTCCTCTGTACATCCCTCAGACGCTGTTTAACTGG 240
Qy 241 AATTTTGAAGTGGAAATCTGCAATGTTTGGCTCATTTACTGACTATCTTTTGTGCACAGCA 300
Db 241 AATTTTGAAGTGGAAATCTGCAATGTTTGGCTCATTTACTGACTATCTTTTGTGCACAGCA 300
Qy 301 TCGTCTACAGATTTGTCCTCATTTAGCTACGATCGATACCACTCAGTTTCAAAACGCTGTG 360
Db 301 TCGTCTACAGATTTGTCCTCATTTAGCTACGATCGATACCACTCAGTTTCAAAACGCTGTG 360
Qy 361 CGTTATAGCAGACAGCACTGGCATCCTGAAATTTGTTGCTCAAAATGGTGGCTGTTTGG 420
Db 361 TCTTATAGGCTCAACACACTGGCATCTGAAGATTGTTGCTCAAAATGGTGGCTGTTTGG 420
Qy 421 ATACTGCTTCTTGGTCAATGGCCCAATGATTTCTGGCTTCGGATTTCTTGGAAACAGC 480
Db 421 ATACTGCTTCTTGGTCAATGGCCCAATGATTTCTGGCTTCGGATTTCTTGGAAACAGC 480
Qy 481 ACCAACACAGAGGAGTCGAGCCTGGCTTTGTTTACTGAGTGGTACATCCTCGCCATTACA 540
Db 481 ACCAACACAGAGGAGTCGAGCCTGGCTTTGTTTACTGAGTGGTACATCCTCGCCATTACA 540
Qy 541 GCATTTTGGAAATTCCTGCTCCCTGCTCCTTGGTGTCTTATTTTCAAGTACAGATTAC 600
Db 541 ATGCTCTTGGAAATTCCTGCTCCTGCTCATCTCTGTGGCTTATTTCAATGTACAGATTAC 600
Qy 601 TGGAGCCTGTGGAGGCTGGGAGTCTCAGTAGGTGGCTTACCGCTAGCCGCTGATTCATCGCT 660
Db 601 TGGAGCCTGTGGAGGCTTAGGGCTCTCAGTAGGTGGCTTACCGCTAGCCGCTGATTCATTCCT 660
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Qy 661 ACCTCTTCCAGGGGCACTGGACACTCAGCGAGAACTGGGTTGGCTTGTAGACAAAGTCTT 720
Db 661 ACCTCTTCCAGTCTCTTACGAGACACTTACACAGAGCTGGGGTGGCTTGCAGACAAAGTAAT 720
Qy 721 CTTGGATTAAAGGAACACGCGCATCCCTTTTATTTCAGAAAGTCCACGAGGAAAGAGCAGT 780
Db 721 CTTGGATTGAAGGAATCAGCTGCATCTCTGCTCACTCAGAAAGTCTCTGAAGAAAGAGCAGC 780
Qy 781 CTCTGCTGTCCTTAAGGACTCAGATGAGCGGTAGTATCATCCCTTTCAAAGTGGGTTC 840
Db 781 ATCTGCTGTCCTTAAGGACTCAGATGAGCGGTAGTATCATCCCTTTCAAAGTGGGTTC 840
Qy 841 TTCTGCGGATCAGAAAGCCAGTGTCTTACCACAGAGAGCACGCTGGAGCTTCTCAGAGGC 900
Db 841 TTCTGGGATCGAAAGTGGAGCGCTTTCGCAAGGAGTACGAGAGCTTCTCAGAGGC 900
Qy 901 AGGAAGCTAGCCAGGTGCGTGTCTCTCTCCTCCTGAGTGTCTTTTGGCCATTTTCTGGGTCCG 960
Db 901 AGGAAGCTAGCCAGGTGCGTGTCTCTCTCCTCCTGAGTGTCTTTTGGCCATTTTCTGGGTCCA 960
Qy 961 TATTGCTGTTCACAAATTTGCTTTTCAACTTATCGCAGAGGAGCGCCCAAAATCGATT 1020
Db 961 TACTGTCTGTTCACAAATTTGCTTTTCAACTTATCGCAGAGGAGCGCCCAAAATCGGTG 1020
Qy 1021 TGGTACAGCATAGCCTTTTGGCTACAGTGTTCAAATTTCACTTATTAATCCCTTCTATAC 1080
Db 1021 TGGTACAGCATAGCCTTTTGGCTACAGTGTTCAAATTTCACTTATTAATCCCTTCTGTAC 1080
Qy 1081 CCTTTGTGCCACAGAGCTTTTCCAGAGGCTTCTTGAAGATATCTGTGTGACAAAGCAA 1140
Db 1081 CCTTTGTGTCCAGAGGCTTTTCCAGAGGCTTCTTGAAGATATCTTTGTGTGACAAAGCAA 1140
Qy 1141 CGAGCACCCTCAGAGACCCAGTCAGTATCTTCTTGA 1176
Db 1141 CGAGCCTGTCCAGAGAACCCAGTCAGTATCTTCTTGA 1176

RESULT 5
US-10-626-126-5
; Sequence 5, Application US/10626126
; Publication No. US20050074770A1
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Liu, Changlu
; TITLE OF INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Subtype
; FILE REFERENCE: PRD-0033
; CURRENT APPLICATION NUMBER: US/10/626,126
; CURRENT FILING DATE: 2003-07-23
; PRIOR APPLICATION NUMBER: 09/790,849
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/208,260
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 1176
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-626-126-5

Query Match      81.5%; Score 958.4; DB 21; Length 1176;
Best Local Similarity 88.4%; Pred. No. 5e-295;
Matches 1040; Conservative 0; Mismatches 136; Indels 0; Gaps 0;

Qy 1 ATGTCGGAGTCTAACGGCACTGAGCTCTTGGCACTGCTGCAAGTCCCTTGGCATTT 60
Db 1 ATGTCGGAGTCTAACGGCACTGAGCTCTTGGCACTGCTGCAAGTCCCTTGGCATTT 60
Qy 61 TTAATGTCCTTGGTCTTGGTCTTGGTCTTGGTCTTGGTCTTGGTCTTGGTCTTGG 120
Db 61 TTAATGTCCTTGGTCTTGGTCTTGGTCTTGGTCTTGGTCTTGGTCTTGGTCTTGG 120
Qy 121 GTAGCAGACAGAAACCTTAGACATCGAAGTAATTTATTTTCTTAATTTGGCTATTCT 180
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	Db	121	GTGTTGGACAGAAACCCTTAGACATCGAAGTAATAATTTTTTTCATTAAATTTGGCTATTTCCT	180
	Qy	181	GACTTCTTCGTGGGTGCATCTCCATTCTCCTGTACATCCCTCACAGCTGTTTTAACTGG	240
	Db	181	GACTTCTCGTGGGTTCGATTTCCATTTCCCTCTGTACATCCCTCACGTTGTGTTTAACTGG	240
	Qy	241	AATTTTGGAAAGTGAAATCTGCATGTTTTGGCTCAATTACTGACTATCTTTTGTGTCACAGCA	300
	Db	241	AATTTTGGAAAGTGAAATCTGCATGTTTTGGCTCAATTACTGACTATCTTTTGTGTCACGCCA	300
	Qy	301	TCCGTCTACAGTATTGTTCCTCATTTAGCTACGATCGATACGATCAGTTCAGAAACGCTGTG	360
	Db	301	TCTGTCTACAATAATGTTCCTCATTTAGCTACGATCGATACGATCAGTTCAGAAACGCTGTG	360
	Qy	361	CGTTATAGACACACGACACTGGGCATCTCAAATAATGTTCCTCAAATGGTGGCTGTTTGG	420
	Db	361	TC TTATAGGGCTCAACACACTGGGCATCATGAAGATTTGTTGCTCAATGGTGGCTGTTTGG	420
	Qy	421	ATACTGGCTTTCTTGGTCAATFGGCCCCAATGANTCTGCTTCGGAATCTTTGGAGAAGAACGC	480
	Db	421	ATACTGGCTTTCTTGGTAAAATGGGCCGATGANTCTGGCTTCAGATTTCTTGGAGAAGAACGC	480
	Qy	481	ACCAACACAGAGAGTGGAGCCTGGCTTTGTTACTGAGTGGTACATCTTCGCCATTACA	540
	Db	481	ACGAACACAAGGACTGTGAGCTGGCTTTGTTACTGAGTGGTACATCTTCGCCATTACA	540
	Qy	541	GCATTCTTGGAAATTTCTTGCTCCCTGTCTCCTTTGGTGGTCTAATTTCAAGTACAGATTTTAC	600
	Db	541	ATGCTCTTGGNAATTCCTGCTCTCTGTCTCATCTCTGTGGCTTAATTTCAATGTACAGNTTAC	600
	Qy	601	TGGAGCTGTGGAAGCGTGGAGGTCTCAGTAGAGTGGCCCTAGCCACGCTGGATTCATCGCT	660
	Db	601	TGGAGCTGTGGAAGCGTGGAGGTCTCAGTAGAGTGGCCCTAGCCATGCTGGATTTCTCCACT	660
	Qy	661	ACCTCTTCCAGGGACCTGGACACTCAGCAGAACTGGTGTGGCTCTGAGACAAAGTCTT	720
	Db	661	ACCTCTTCCAGTGTCTCAGGACACTTACACAGACTGGGTGGCTTGACGACAAAGTAAAT	720
	Qy	721	CCTGGATTAAAGGAACACAGCCGCATCCCTTCATTTCAGAAAACTCACAGAGAAAGACGAGT	780
	Db	721	CCTGGATTGAAGGAATCAGCTGCATCTCGTCACTCAGAAAGTCTTCGAGAAAGACGAGC	780
	Qy	781	CTCTGTGTGCTTTAAGACTCATCATGAGCGGTAGTATCATCGCCTTCAAAGTGGGTTC	840
	Db	781	ATCTGTGTGCTTTAAGACTCATCATGAACAGCAGTATCACTGCGCTTCAAAGTGGGTTC	840
	Qy	841	TTCTGCCGATCAGAAAGCCCAGTCTTCCACGAGAGAGACGCTGGAGCTTCTCAGAGGC	900
	Db	841	TTCTGGCGATCGSAAAGTGCAGCGCTTCGCCAAAGGGAGTACGACAGCTTCTCAGAGGC	900
	Qy	901	AGGAAGCTAGCCAGGTCCGTAGCTGTCTCTCGAGTGTCTTTGCGCATTTGCTGGGCTCCG	960
	Db	901	AGGAAGCTAGCCAGGTCACTGGCCATCTTCTGAGCGCTTTTGCCATTTGCTGGGCTCCA	960
	Qy	961	TATPGCTGTGTACAAATGTGTTCTTTCAACTPATCCGAGAGGGAGCGCCCCAAATCGATT	1020
	Db	961	TACTGTCTGTTCACAAATGTCTTCAACTTACCCCGAAGACGAAACGCCCAATCGGTG	1020
	Qy	1021	TGGTACAGCATAGCCTTTTGGCTACAGTGGTTCAAATTCATTTAATCCCTTTCTATAC	1080
	Db	1021	TGSTACAGCATTGCCTTCTGGCTGCATGGTTCAAATTCGTTTGTGTTAATCCCTTTCTGTAC	1080
	Qy	1081	CCTTTGTGCCACACAGCTTTCCAGAAGCTTTCTTGGAAAGTACTCTGTGTGACAAAGCAA	1140
	Db	- 1081	CCTTTGTGTACAGCGTTTCCAGAAGCTTTCTTGGAAAGTACTCTTGTGTGACAAAGCAA	1140
	Qy	1141	CCAGCACTTCCACAGACCCAGTCAAGTATCTTCTTGA	1176
	Db	1141	CCAGCGTGTCCAGAAACCACTCAGTATCTTCTTGA	1176

## RESULT 6

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US-10-626-398-5
; Sequence 5, Application US/10626398
; Publication No. US20050074841A1
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Liu, Changlu
; TITLE OF INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Subtype
; FILE REFERENCE: PRD-0034
; CURRENT APPLICATION NUMBER: US/10/626,398
; CURRENT FILING DATE: 2003-07-23
; PRIOR APPLICATION NUMBER: 09/790,849
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/208,260
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 1176
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-626-398-5

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Query Match	81.5%;	Score 958.4;	DB 21;	Length 1176;
Best Local Similarity	88.4%;	Pred. No. 5e-295;		

Qy	1	ATGTCGAGTCTAACGGCACTGACGTCCTTGCCACTGACTGCTCAAGTCCCTCTGGCAATT	60
Db	1	ATGTCGAGTCTAACAGTACTGGCAGTCCTTGCCACAGCTGCTCAGGTCCCTCTGGCAATT	60
Qy	61	TTAATGTCCTGCTTGCTTTGCTATAAACATAGGCAATGCTGTGGTCAATTTAGCCCTTT	120
Db	61	TTAATGTCCTCAATTTGGCTTTGCTATTAATGGTAGGCAATGCTGTGGTCACTTTAGCCCTTT	120
Qy	121	GTAGCAGACAGAAACCTTAGACATCGAAGTAATTAATTTTTTTCTTAATTTGGCTATTTC	180
Db	121	GTGGTGACAGAAACCTTAGACATCGAAGTAATTAATTTTTTTCTTAATTTGGCTATTTC	180
Qy	181	GACTTCTCTGGGGTGTCATCTCCATTCCTGTGACATCCCTCACACGCTGTTTAACCTGG	240
Db	181	GACTTCTCTGGGGTTGATTTCCATTCCTGTGACATCCCTCACGCTGTTGTTAACTGG	240
Qy	241	AAATTTTGGAAAGTGGAAATCTGCATGTTTTGGCTCAATTAAGTACTATCTTTGTGCACAGCA	300
Db	241	AAATTTTGGAAAGTGGAAATCTGCAATGTTTTGGCTCAATTAAGTACTATCTTTGTGCACCGCA	300
Qy	301	TCGGTCTACAGTATTGTCTCATTTAGCTACGATCGATACCAAGTCAGTTTCAAACGCTGTG	360
Db	301	TCTGTCTACAAATATTGTCTCATTTAGCTACGATCGATACCAAGTCAGTTTCAAATGCTGTG	360
Qy	361	CGTTTATAGACACAGCACACTGGCATCTCGAAATTTGTTGCTCAAAATGGTGGCTGTTTGG	420
Db	361	TCATTATAGGCTCAACACACTGGCATCATGAAGATTGTTGCTCAAAATGGTGGCTGTTTGG	420
Qy	421	ATACTGGCTTTCTTGTTCAATGGCCCAATGATTTCTGGCTTCGGATTCTTGGGAAGAACGC	480
Db	421	ATACTGGCTTTCTTGTTAAATGGCCCGATGATTTCTGGCTTCAGATTCTTGGGAAGAACGC	480
Qy	481	ACCAACACAGAGGATCGAGCCTGGCTTTGTTACTGAGTGGTACATCTCTCGCCATTACA	540
Db	481	ACGAAACAAAGGACTGTGAGCCTGGCTTTGTTACAGATGGTACATCTCTCACCATTACA	540
Qy	541	GCAATTTCTGGAAATTCCTGCTCCCTGTCCTCTGGTGGTCTATTTCAGTGTACAGATTTC	600
Db	541	ATGCTCTTGGAAATTCCTGCTTCCTGTCATCTCTGTGGCTTATTTCAAATGTACAGATTTC	600
Qy	601	TGGAGCTGTGGGAAGCGTGGGAGTCTCAGTAGGTGCCCTAGCCACGCTGGATTTCATCGCT	660
Db	601	TGGAGCTGTGGGAAGCGTAGGGCTCTCAGTAGGTGCCCTAGCCATGCTGGATTTCCTCACT	660
Qy	661	ACCTCTTCCAGGGGCACTGGACACTACGAGAACTGGGTTGGCTTTGTAGGACAAGTCTT	720
Db	661	ACCTCTTCCAGTGTCTCAGACACTTACACAGAGCTGGGTGGCTTGCAGACAGAGTAAT	720

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Qy 721 CCTGGATTAAAGGACAGCGCATCCCTTCATTTCAGAAAGTCCACGAGGAAGAGCAGT 780
Db 721 CCTGGATTGAAGGAATCAGCTGCTCTCGTCACTCAGAAAGTCCTCGAGAAAGAGCAGC 780
Qy 781 CTCTGTGTCTTAAAGGACTCACATGAGCGGTAGTATCATCGCTTCAAAGTGGGTTC 840
Db 781 ATCTGTGTCTTAAAGGACTCACATGAAAGCGATCATCTGCTTCAAAGTGGGTTC 840
Qy 841 TTCTGCCGATCAGAAAGCCAGCTCTTCCACGAGAGAGCAGCGTGGAGCTTCTCAGAGGC 900
Db 841 TTCTGCCGATCGGAAAGTCAAGCGCTTCCGCAAGAGGAGTACGACAGAGCTTCTCAGAGGC 900
Qy 901 AGAAGCTAGCCAGGTGCTAGTCTCTCTGAGTGTCTTTCGCAATTTGCGGCTCCG 960
Db 901 AGAAGCTAGCCAGGTCACTGCGCATCTCTGAGCGCTTTTGCAATTTGCTGGGCTCCA 960
Qy 961 TATTGCTGTTCACAAATGTTCTTCAACTTATCGCAGAGGGGAGCGCCCAAAATCGATT 1020
Db 961 TACTGTCTGTTCACAAATGTTCTTCAACTTATCCCAAGAGCGGACGCCCCAAATCGGTG 1020
Qy 1021 TGGTACAGTACAGCTTTTGGCTACAGTGGTTCAAATTCATTAATCCCTTTCTATAC 1080
Db 1021 TGGTACAGTATGCTTCTGGCTGCAATGGTTCAAATTCGTTTGTAAATCCCTTTCTGTAC 1080
Qy 1081 CCTTGTGCCACAGACGTTTCCAGAGGCTTCTGGAAGATACCTGCTGTGACAAAGCAA 1140
Db 1081 CCTTGTGTACAGAGGCTTCCAGAGGCTTCTGGAAGATACCTTGTGACAAAGCAA 1140
Qy 1141 CCAGCACCTTCCAGAGCCAGTCACTATCTTCTTGA 1176
Db 1141 CCAGCGTGTCCAGAACCACTGATCTCTTGA 1176
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## RESULT 7

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US-09-812-216-1
; Sequence 1, Application US/09812216
; Patent No. US20020098539A1
; GENERAL INFORMATION:
; APPLICANT: Behan, Jiang Xu
; APPLICANT: Hedrick, Joseph A.
; APPLICANT: Laz, Thomas M.
; APPLICANT: Monema, Frederick J. Jr.
; APPLICANT: Morse, Kelley L.
; APPLICANT: Umland, Shelby P.
; APPLICANT: Wang, Suke
; TITLE OF INVENTION: Histamine receptor
; FILE REFERENCE: CN01069
; CURRENT APPLICATION NUMBER: US/09/812,216
; CURRENT FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: 09/414,010
; PRIOR FILING DATE: 1999-10-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-812-216-1
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Query Match 56.9%; Score 669; DB 9; Length 1173;
Best Local Similarity 74.2%; Pred. No. 1.7e-202;
Matches 875; Conservative 0; Mismatches 295; Indels 9; Gaps 2;
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Qy 1 ATGTCGAGTCTAAGGCACTGACGCTCTGCGCACTGACTGCTCAAGTCCCTTGGCAATTT 60
Db 1 ATGCGAGATCAATAGACAAATCAATTAATCACTAAGCACTCGTGTACTTTAGCAATTT 60
Qy 61 TTAATGTCCTGCTGCTTTTGGCTTAAAGTACGATAGGCAATGCTGTGGTCAATTTAGCCTTT 120
Db 61 TTTATGTCCTTAGTAGCTTTTGGCTTAAATGCTAGGAAATGCTTTGGTCAATTTAGCTTTT 120
Qy 121 GTAGCAGACAGAAACCTTAGACATCGAAGTAATTAATTTTCTTAATTTGGCTATTCT 180
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Db 121 GTGTGGACAAAAAACCCTTAGACATCGAAGTAGTTATTTTTTCTTAACCTTGGCACTCT 180
Qy 181 GACTTCTTCGTGGGTGTCTATCTCCATTTCCCTGTGTACATCCCTCACAGCTGTTTAACTGG 240
Db 181 GACTTCTTCGTGGGTGTGTATCTCCATTTCCCTTGTGTACATCCCTCACAGCTGTTTAACTGG 240
Qy 241 AATTTTGAAGTGGAAATCTGCATGTTTGGCTCATTAATCTGACTATCTTTTGTGACAGCA 300
Db 241 GATTTTGGAAAGGAAATCTGTGTATTTTGGCTCACTACTGACTATCTGTGTATGTACAGCA 300
Qy 301 TCCGTCTACAGTATGCTCTCTCATTTAGTACGATACCGATACCGTGTGCTTCAAAGCTGTG 360
Db 301 TCTGTATATAACATGTTCTCTCATCAGCTATGATCGATACCTGTGCTCAATATGCTGTG 360
Qy 361 CGTTATAGAGCACAGCACACTGGCATCTCGAAAAATTTTGTCTCAAAATGGTGGCTTTGG 420
Db 361 TCTTATAGAACTCAACATACCTGGGTCTTGAAGATTTTACTCTGATGGTGGCGGTTTGG 420
Qy 421 ATACTGGCTTCTTGTGTCAATGCGCCCAATGATTTCTGGCTTCGGATTTCTTGAAGACAGC 480
Db 421 GTCTTGGCTTCTTGTGTCAATGCGCCCAATGATTTCTAGTTTTCAGAGTCTTGAAGAGCA 476
Qy 481 ACCAACACAGAGGAGTGGAGCGCTGCTTTGTGTACTCTGAGTGTGTACATCTCTCGCATTT 540
Db 477 --TGAAGTAGTGAATGTGTGACCTGATTTTTCGGAATGGTACATCTCTGCGCATTCACA 534
Qy 541 GCATTTCTTGGAAATCTCTGCTCTCTGCTCTCTGCTCTCTGCTCTCTGCTCTCTGCTCTCT 600
Db 535 TCATTTCTTGGAAATCTCTGCTCTCTGCTCTCTGCTCTCTGCTCTCTGCTCTCTGCTCTCT 594
Qy 601 TGGAGCTGTGGAAGCGTGGAGTCTCAGTAGTGTGCTTACCTAGTGTGCTTACCTAGTGTG 660
Db 595 TGGAGCTGTGGAAGCGTGGATCATCTCAGTAGTGTGCAAGCCATCTCTGAGTGTGCTCT 654
Qy 661 ACCTTCTTCCAGGGGCACTGACACTCAACGAGAACTGGGTTGGCTGTGTAGACAAAGTCTT 720
Db 655 GTCTTCTTCCAACTCTGTGTGACACTCATTTCAAGAGGTAGACTATCTTCAAGAGATCTCT 714
Qy 721 CCTGGATTAAAGAAACGAGCGCATCCCTTCATTTCAGAAAGTCCACGAGGAAGAGCAGT 780
Db 715 TCTGCTATCGACAGAAAGTTCCTGCTATCTTCAATTCAGAGAGACAGAGGAGAGAGTAGT 774
Qy 781 CTCTGTGTCTTAAAGGACTCACATGAGCGGTAGTATCATCGCTTCAAAGTGGGTTC 840
Db 775 CTATGTTTCTTCAAGAACCAAGATGAATAGCAATACAATTTGCTTCCAAAAATGGGTTC 834
Qy 841 TTCTGCGCATCAGAAAGCCAGTGTCTTCCACAGAGAGACAGCTGGAGCTTCTCAGAGGC 900
Db 835 TTCTTCCAACTCAGATTCGTAGCTTCTCACCAGGAGGAACTGTTGAACCTGTAGAGCC 894
Qy 901 AGAAGCTAGCCAGGTGCTGCTGCTCTCTGAGTGTCTTTTGGCAATTTGCTGGGCTCCG 960
Db 895 AGGAGATTAGCCAAAGTCACTGGGCAATCTCTTAGGGGTTTTTGTGCTGTGCTGGGCTCCA 954
Qy 961 TATTGCTGTTCACAAATGTTCTTCAACTTATCGCAGAGGGGAGCGCCCAATCGATT 1020
Db 955 TATTCTGTTCACAAATGTTCTTCAATTTATTTCTCAGCAACAGAGTCTCTAAATCAGTT 1014
Qy 1021 TGGTACAGTACAGCTTTTGGCTACAGTGGTTCAAATTCACCTTATTAATCCCTTTCTATAC 1080
Db 1015 TGGTATAGAATTCATTTTGGCTTCAAGTGTTCATTTCTTGTCAATCTCTTTTGTAT 1074
Qy 1081 CCTTTGTGCCACAGAGCTTTTCCAGAGGCTTTTCTGGAAGATACCTGTGTGACAAAGCAA 1140
Db 1075 CCATTTGTGTACAGAGGCTTTTCAAAAGGCTTTCTGAAAAATATTTTGTATAAAAAGCAA 1134
Qy 1141 CCAGCACCTTC---ACAGACCGAGTCACTATCTTCTTGA 1176
Db 1135 CCTCTACCATCAACACACAGTCCGTGATCTCTTTAA 1173
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RESULT 8



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US-09-910-411-1
; Sequence 1, Application US/09910411
; Patent No. US20020137054A1
; GENERAL INFORMATION:
; APPLICANT: Bergsma, Derk
; APPLICANT: Fitzgerald, Laura
; APPLICANT: Li, Xiatong
; APPLICANT: Michalovich, David
; APPLICANT: Zhu, Yuan
; TITLE OF INVENTION: AXOR35, A G-Protein Coupled Receptor
; FILE REFERENCE: GP70655-2C1
; CURRENT APPLICATION NUMBER: US/09/910,411
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: 09/693,761
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 09/497,790
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/431,898
; PRIOR FILING DATE: 1999-11-02
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-910-411-1

Query Match      56.9%; Score 669; DB 9; Length 1173;
Best Local Similarity 74.2%; Pred. No. 1.7e-202;
Matches 875; Conservative 0; Mismatches 295; Indels 9; Gaps 2;

Qy 1 ATGTCGAGTCTAACGGCACTGACGCTCTGCGCACTGACTGCTCAAGTCCCTTGCCATT 60
Db 1 ATGCGAGATATAATAGCACAAATTAATTAATCACTAAGCACTCTGTTACTTTAGCAATT 60
Qy 61 TTAATGTCCTGCTTCTTTGCTTATACGATAGCAATGCTGTTGGTCAATTTAGCCCTT 120
Db 61 TTTATGCTCTAGTAGCTTTTGTCTATAATGCTAGGAAATGCTTTGGTCAATTTAGCTTT 120
Qy 121 GTAGCAGACAGAAACCTTAGACATCGAAGTAATTTATTTTCTTAATTTGGCTATTCT 180
Db 121 GTGCTGACAAAACCTTAGACATCGAAGTAGTATTTTCTTAATTTGGCCATCTCT 180
Qy 181 GACTTCTTGGGGTGATCTCCATTCCTTTGATACATCCCTCACAGCTGTTTGAATGG 240
Db 181 GACTTCTTGGGGTGATCTCCATTCCTTTGATACATCCCTCACAGCTGTTTGAATGG 240
Qy 241 AATTTTGGAGTGAATCTGATCTTTTGGCTCAATTAAGTACTGACTATCTTTGTCACAGCA 300
Db 241 GATTTTGGAAAGGAAATCTGTGTTTGGCTCACTACTGACTATCTGTTATGTACAGCA 300
Qy 301 TCCGCTACAGTATTGCTCTCATTTAGCTACGATCGATACCACTCAGTTTCAACCGCTGTG 360
Db 301 TCTGTATATACATTTGCTCTCATCGATATGATCGATACCTGTCAGTCTCAATGCTGTG 360
Qy 361 CGTTATAGACACAGCACTGGCATCCTGAAATTTGTTGCTCAAAATGGTGGCTGTTGG 420
Db 361 TCTTATAGAACTCAACATCTAGTGGGTCTTGAAGATTGTTACTCTGATGTTGGCGTGGT 420
Qy 421 ATACTGCTTTCTTGGTCAATGGCCCAATGATTTGGCTTCGGATTCTTGGAAACAGC 480
Db 421 GTGCTGGCTCTTTAGTGAATGGGCCAATGATTTCTAGTTTCAGAGTCTTGGAAAGCA 476
Qy 481 ACCAACACAGAGGAGTGGAGCCCTGGCTTTCTTACTGAGTGTATCATCTCGCCATTACA 540
Db 477 --TGAAGGTAGTGAATGTGAACCTGGATTTTTCGGAAATGATACCTTGGCCATACA 534
Qy 541 GCATTCTTGGAAATCTCTGCTCCCTGCTCTTGGTGGTCTATTTTTCAGTGTACAGATTAC 600
Db 535 TCATTCTTGGAAATCTGATGCCAGTCTTATTTAGTGGCTTATTTTCAACATGAATTTAT 594
Qy 601 TGGAGCCTGTGGAAGCGTGGAGTCTCTAGTAGTGGCTTACCGACGCTGGATTCTATCGCT 660
Db 601 TGGAGCCTGTGGAAGCGTGGAGTCTCTAGTAGTGGCTTACCGACGCTGGATTCTATCGCT 660
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Db 595 TGGAGCCTGTGGAAGCGTGTATCTCTCAGTAGGTGCGCAAGCCATCTCGGACTGACTGCT 654
Qy 661 ACCTCTTCCAGGGGCACTGGACACTCAGCAGAACTGGGTTGGCTTGTAGGACAACTCT 720
Db 655 GTCTCTTCCAACTCTCTGGACACTCATTAGAGGTAGACTATCTTCAAGAGATCTCTT 714
Qy 721 CTTGATTTAAAGAACCCAGCGCATCTCTTCAATTCAGAAAGTCCACGAGGAAAGAGCAGT 780
Db 715 TCTGATCGACAGAAAGTCTCTGCACTCTCTTCAATTCAGAGAGACAGAGGAAAGAGTAGT 774
Qy 781 CTCTGTGTCTTAAAGGACTCACATGAGCGGTAGTATCATCGCTTCAAAAGTGGTTCC 840
Db 775 CTATGTTTCTTCAAGAACCAAGATGAATAGCAATCAATTTCTTCAAAATGGGTTCC 834
Qy 841 TTCTGCGATCAGAAAGCCAGTCTCTTCCAGAGAGACGAGTGGAGCTTCTCAGAGGC 900
Db 835 TTCTCCCAATCAGATTCTGTAGCTCTTCCACAAAGGAAACATGTTGAACCTCTTAGAGCC 894
Qy 901 AGGAAGTACGCGAGTCTGCTAGTCTCTCTGAGTGTCTTGGCATTTGCTGGGCTCG 960
Db 895 AGGAGATTAGCCAAAGTCACTGGCCATTCTCTTAGGGGTTTTTGTGCTGTGGGCTCCA 954
Qy 961 TATTGCTGTTCACAAATTTGTTTCAACTTATCGCAGAGGGAGCGCCCAATCGATT 1020
Db 955 TATTCTCTTTCACAAATTTGCTTCAATTTATTTCTCAGCAACAGGTCCTAAATCAGTT 1014
Qy 1021 TGGTACAGCATAGCTTTTGGCTACAGTGGTTCAAATTCACATTATTAATFCCCTTCTATAC 1080
Db 1015 TGGTATAGAAATGCAATTTGGCTTCACTGGTTCATTTCTTGTCAATCTCTTTTGTAT 1074
Qy 1081 CTTTGTGTCACAGACGTTTCCAGAGGCTTTCTGGAAGATACCTCTGTGTGACAAAGCAA 1140
Db 1075 CCATTGTGTACAGAGCGCTTCAAAAGGCTTCTTGAATAATTTTGTATATAAAGCA 1134
Qy 1141 CCAGCACCTTC--ACAGACCCAGTCACTATCTTCTGA 1176
Db 1135 CCTCTACATCAACACAGCTCGGTCACTATCTTCTTAA 1173

RESULT 9
US-09-875-076-13
; Sequence 13, Application US/09875076
; Publication No. US20030017528A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Dang, Huong T.
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
; FILE REFERENCE: AREN0050
; CURRENT APPLICATION NUMBER: US/09/875,076
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 09/417,044
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,851
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/123,946
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,949
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/136,436
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,437
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,439
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,567
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/137,127
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/137,131
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PRIOR FILING DATE: 1999-05-28  
PRIOR APPLICATION NUMBER: 60/141,448  
PRIOR FILING DATE: 1999-06-29  
PRIOR APPLICATION NUMBER: 60/156,653  
PRIOR FILING DATE: 1999-09-29  
PRIOR APPLICATION NUMBER: 60/156,633  
PRIOR FILING DATE: 1999-09-29  
PRIOR APPLICATION NUMBER: 60/156,555  
PRIOR FILING DATE: 1999-09-29  
PRIOR APPLICATION NUMBER: 60/156,634  
PRIOR FILING DATE: 1999-09-29  
PRIOR APPLICATION NUMBER: 60/157,280  
PRIOR FILING DATE: 1999-10-01  
PRIOR APPLICATION NUMBER: 60/157,294  
PRIOR FILING DATE: 1999-10-01  
PRIOR APPLICATION NUMBER: 60/157,281  
PRIOR FILING DATE: 1999-10-01  
PRIOR APPLICATION NUMBER: 60/157,293  
PRIOR FILING DATE: 1999-10-01  
PRIOR APPLICATION NUMBER: 60/157,282  
PRIOR FILING DATE: 1999-10-01  
NUMBER OF SEQ ID NOS: 74  
SOFTWARE: Patent in Ver. 2.1  
SEQ ID NO 13  
LENGTH: 1173  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-875-076-13

Query Match 56.9%; Score 669; DB 10; Length 1173;

Best Local Similarity 74.2%; Pred. No. 1.7e-202;

Matches 875; Conservative 0; Mismatches 295; Indels 9; Gaps 2;

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Qy 1 ATGCGAGCTAAGGCACTGAGCTCTTGCCACTGACTGCTCAAGTCCCTTGGCAATTT 60
Db 1 ATGCGAGCTAAGGCACTGAGCTCTTGCCACTGACTGCTCAAGTCCCTTGGCAATTT 60
Qy 61 TTAATGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
Db 61 TTAATGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
Qy 121 GTACAGACAGAAACCTTAGACATCGAAGTAATTTTCTTAATTTGGCTATTCT 180
Db 121 GTGCGGACAAAACCTTAGACATCGAAGTAATTTTCTTAATTTGGCCATCTCT 180
Qy 181 GACTTCTTGGGTGCTCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
Db 181 GACTTCTTGGGTGCTCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
Qy 241 AATTTTGGAAAGTGAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
Db 241 AATTTTGGAAAGTGAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
Qy 301 TCGCTTACAGTATTGCTCCTCATTAGCTAGCATGATGATGATGATGATGATGATG 360
Db 301 TCGTATATAACATTGCTCCTCATTAGCTAGCATGATGATGATGATGATGATGATG 360
Qy 361 CGTTATAGACAGACAGCATGCGCATCTGGAATTTGCTGCTGCTGCTGCTGCTGCT 420
Db 361 TCTTATAGAACTCAACATCTGCGGCTCTGGAATTTGCTGCTGCTGCTGCTGCTG 420
Qy 421 ATACTGCTTCTTGGTCAATGCGCCCAATGATTTCTGCTGCTGCTGCTGCTGCTG 480
Db 421 GTGCTGCTTCTTGGTCAATGCGCCCAATGATTTCTGCTGCTGCTGCTGCTGCTG 476
Qy 481 ACCAACAGAGGAGTGGAGCCTGGCTTTGTTACTGAGTGGTACATCTCGCCATTACA 540
Db 477 --TGAAGGTAGTGAATGTGAACCTGGATTTTTTTCGGAAATGATACATCTTGC 534
Qy 541 GCATTCTTGGAAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
Db 535 TCATTCTTGGAAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 594
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Qy 601 TGGAGCTGTGGAAGCGTGGAGTCTCAGTAGTGCCCTAGCCACGCTGGATTTCATGCT 660
Db 595 TGGAGCTGTGGAAGCGTGGATCATCTCAGTAGTGCCCAAGCCATCTGGACTGCTGCT 654
Qy 661 ACCTTTCCAGGGGCACTGGACACTCACGAGAACTGGGTGGCTTTGAGGACAACTTT 720
Db 655 GTCTCTTCCAACTCTGTGGACACTCATTCAGAGGTAGACTATCTTTCAAGGAGATCTCT 714
Qy 721 CTGGATTAAAGGAAACAGCCGATCCCTTCATTTCAGAAAGTCCAGGAGGAAGAGCT 780
Db 715 TCTGCATCGACAGAACTTCTGCACTCTTTCATTTCAGAGAGAGAGGAGAGAGTAGT 774
Qy 781 CTCTGCTGTCTTAAAGGACTCATGAGCGGTAGTATCATCGCTTCAAAAGTGGGTTC 840
Db 775 CTCAATGTTTCTCAAGAACCAAGATGAATAGCAATACAAATGCTTCCAAAATGGGTTC 834
Qy 841 TTCTGCCGATCAGAAAGCCAGTGTTCACAGAGAGAGACGTCGAGCTTCTCAGAGGC 900
Db 835 TTCTCCAAATCAGATTTCTGTAGCTTTCACAAAGGAAACATGTTGAATGCTTTAGAGCC 894
Qy 901 AGGAAGTAGCAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
Db 895 AGGAGATTAGCCAAAGTCACTGGCCATTTCTTTAGGGGTCTTTGCTGCTGCTGCTG 954
Qy 961 TATTGCTGTTTCAAAATTTGTTCTTCAACTTATCGCAGAGGGAGCGCCCAATCGATT 1020
Db 955 TATTCTGTTTCAAAATTTGCTTTCATTTTATTCCTCAGCAACAGGTCTCTTAATCAGTT 1014
Qy 1021 TGCTCAGCATAGCTTTTGGCTTACAGTGGTTCAAATTCATTTAATTCCTTTTCTATAC 1080
Db 1015 TGCTATAGAAATTCATTTTGGCTTTCAGTGGTTCAAATTCCTTTGCTCAATCTCTTTGTAT 1074
Qy 1081 CTTTGTGCGACAGAGTTCAGAAAGGCTTCTGGAAGGCTTCTGGAAGATCTCTGTGACAAAGCAA 1140
Db 1075 CCATTGTGTCACAGCGCTTTCAAAAGGCTTCTTGAATAATTTGTTATATAAAGCAA 1134
Qy 1141 CCAGCACCTTC--ACAGACCCAGTCAGTATCTTCTTGA 1176
Db 1135 CCTTACCATCACAAACAGTCGGTCAGTATCTTCTTAA 1173
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## RESULT 10

US-09-876-252-13

; Sequence 13, Application US/09876252

; Publication No. US20030018182A1

; GENERAL INFORMATION:

; APPLICANT: Behan, Dominic P.

; APPLICANT: Lehmann-Bruinsma, Karin

; APPLICANT: Chalmers, Derek T.

; APPLICANT: Lowitz, Kevin P.

; APPLICANT: Lin, I-Lin

; APPLICANT: Dang, Huong T.

; APPLICANT: Chen, Ruoping

; APPLICANT: Liaw, Chen W.

; TITLE OF INVENTION: Non-Endogenous Constitively Activated Human G Protein Coupled Rec

; FILE REFERENCE: AREN-0054

; CURRENT APPLICATION NUMBER: US/09/876,252

; CURRENT FILING DATE: 2001-06-07

; PRIOR APPLICATION NUMBER: 09/416,760

; PRIOR FILING DATE: 1999-10-12

; PRIOR APPLICATION NUMBER: 09/170,496

; PRIOR FILING DATE: 1998-10-13

; PRIOR APPLICATION NUMBER: 60/110,060

; PRIOR FILING DATE: 1998-11-27

; PRIOR APPLICATION NUMBER: 60/120,416

; PRIOR FILING DATE: 1999-02-16

; PRIOR APPLICATION NUMBER: 60/121,852

; PRIOR FILING DATE: 1999-02-26

; PRIOR APPLICATION NUMBER: 60/109,213

; PRIOR FILING DATE: 1998-11-20

; PRIOR APPLICATION NUMBER: 60/123,944

; PRIOR FILING DATE: 1999-03-12

; PRIOR APPLICATION NUMBER: 60/123,945





; CURRENT APPLICATION NUMBER: US/10/052.193  
; CURRENT FILING DATE: 2002-01-17  
; PRIOR APPLICATION NUMBER: 0101223.6  
; PRIOR FILING DATE: 2001-01-17  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 1173  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-052-193-1

Query Match 56.9%; Score 669; DB 13; Length 1173;  
Best Local Similarity 74.2%; Pred. No. 1.7e-202; Mismatches 295; Indels 9; Gaps 2;  
Matches 875; Conservative 0;

Qy 1 ATGTGGAGCTTAACGGCACTGAGCTCTTCCCACTGCTCAAGTCCCTTGGCAATTT 60  
Db 1 ATGCCAGATACATAAGCACAATCAATTTATCACTAAGCACTCGTGTACTTTAGCAATTT 60

Qy 61 TTAATGTCCTGCTGCTTCTTCTTCTATTAACATAGGCAATGCTGTGGTCAATTTAGCCTTT 120  
Db 61 TTTATGTCCTTAGTCTTCTTCTTCTTCTATTAACATAGGCAATGCTGTGGTCAATTTAGCCTTT 120

Qy 121 GTAGCAGACAGAAACCTTAGACATCGAAGTAATTTATTTTCTTAATTTGGCTATTTCT 180  
Db 121 GTGGTGACAAAACCTTAGACATCGAAGTAATTTATTTTCTTAATTTGGCTATTTCT 180

Qy 181 GACTTCTTCGTGGGTGATCTCCATTCCTCTGACATCCCTCAACGCTGTTTAACTGG 240  
Db 181 GACTTCTTCGTGGGTGATCTCCATTCCTCTGACATCCCTCAACGCTGTTTAACTGG 240

Qy 241 AATTTTGGAGTGAATCTGCAATGCTGCTGCTCACTACTGACTATCTGTTATGTGACAGCA 300  
Db 241 GATTTTGGAGTGAATCTGCTGCTGCTCACTACTGACTATCTGTTATGTGTTAGTACAGCA 300

Qy 781 CTCTGTGTCTTAAAGCACTCAATGCGGTAGTATCATCGCTTCAAGTGGTTC 840  
Db 781 CTCTGTGTCTTAAAGCACTCAATGCGGTAGTATCATCGCTTCAAGTGGTTC 840

Qy 775 CTCATGTTTTCTCAAGAACCAAGATGAATAGCAATACAAATTTGCTTCCAAATGGTTC 834  
Db 775 CTCATGTTTTCTCAAGAACCAAGATGAATAGCAATACAAATTTGCTTCCAAATGGTTC 834

Qy 841 TTCTGCCGATCAGAAAGCCAGTCTCTTCCAGAGAGAGCACTGGAGCTTCTCAGAGGC 900  
Db 841 TTCTGCCGATCAGAAAGCCAGTCTCTTCCAGAGAGAGCACTGGAGCTTCTCAGAGGC 900

Db 835 TTCTCCCAATCAGATTTCTGTAGCTCTTCCAAAGGGAACATGTTGAACCTGCTTAGAGCC 894  
Qy 901 AGGAAGCTAGCCAGGTCGTAGCTGCTCCTCCTGAGTGTCTTTGCCAATTTGCTGGGTCCG 960  
Db 895 AGGAGATTAGCCAAAGTCACTGGCCATTTCTTAGGGGTTTTTGTCTGTTGCTGGGTCCA 954  
Qy 961 TATTGCTGTTTCAATTTGTTCTTTTCAACTATCGCAGAGGGGAGCGCCCAATCGATT 1020  
Db 955 TATTGCTGTTTCAATTTGTTCTTTTCAACTATCGCAGAGGGGAGCGCCCAATCGATT 1014  
Qy 1021 TGCTACAGCATAGCCTTTTGGCTACAGTGTGTTCAATTTCACTTATTAATCCCTTTCTATAC 1080  
Db 1015 TGCTATAGAAATGCAATTTTGGCTTCAAGTGTGTTCAATTTCTTGTCAATCTCTTTGTAT 1074  
Qy 1081 CCTTTGTGCCACAGAGCTTTTCCAGAGGCTTTCTGGAAGATACCTGTGTGACAAAGCAA 1140  
Db 1075 CCATTGTGTCAAGGCTTTCAAGAGGCTTTCTTGAATAATTTTGTATATAAAGCAA 1134  
Qy 1141 CGAGCACCTTC---ACAGACCCAGTCAGTATCTTCTGA 1176  
Db 1135 CCTTACCATCACAACACAGTCGGTCAGTATCTTCTTAA 1173

## RESULT 12

US-10-290-078-26  
; Sequence 26, Application US/10290078  
; Publication No. US20030124596A1  
; GENERAL INFORMATION:  
; APPLICANT: Carroll, Joseph A.  
; TITLE OF INVENTION: Methods and Compositions for Treating  
; Hematological Disorders Using 232, 2059, 10630, 12848, 13875,  
; TITLE OF INVENTION: 14395, 14618, 17692 or 58874  
; FILE REFERENCES: MPI2001-288P1(M)  
; CURRENT APPLICATION NUMBER: US/10/290, 078  
; NUMBER OF SEQ ID NOS: 27  
; CURRENT FILING DATE: 2002-11-07  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 26  
; LENGTH: 1173  
; TYPE: DNA  
; ORGANISM: Homo sapien  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)...(1173)  
US-10-290-078-26

Query Match 56.9%; Score 669; DB 15; Length 1173;  
Best Local Similarity 74.2%; Pred. No. 1.7e-202; Mismatches 295; Indels 9; Gaps 2;  
Matches 875; Conservative 0;

Qy 1 ATGTGGAGCTTAACGGCACTGAGCTCTTCCCACTGCTCAAGTCCCTTGGCAATTT 60  
Db 1 ATGCCAGATACATAAGCACAATCAATTTATCACTAAGCACTCGTGTACTTTAGCAATTT 60

Qy 61 TTAATGTCCTGCTGCTTCTTCTTCTATTAACATAGGCAATGCTGTGGTCAATTTAGCCTTT 120  
Db 61 TTTATGTCCTTAGTCTTCTTCTTCTATTAACATAGGCAATGCTGTGGTCAATTTAGCCTTT 120

Qy 121 GTAGCAGACAGAAACCTTAGACATCGAAGTAATTTATTTTCTTAATTTGGCTATTTCT 180  
Db 121 GTGGTGACAAAACCTTAGACATCGAAGTAATTTATTTTCTTAATTTGGCTATTTCT 180

Qy 181 GACTTCTTCGTGGGTGATCTCCATTCCTCTGACATCCCTCAACGCTGTTTAACTGG 240  
Db 181 GACTTCTTCGTGGGTGATCTCCATTCCTCTGACATCCCTCAACGCTGTTTAACTGG 240

Qy 241 AATTTTGGAGTGAATCTGCAATGCTGCTGCTCACTACTGACTATCTTTTGTGACAGCA 300  
Db 241 GATTTTGGAGTGAATCTGCTGCTGCTCACTACTGACTATCTTTTGTGTTAGTACAGCA 300

Qy 301 TCCTGCTTACAGTATTTGCTCTTATTTAGTACGATCCAGTCAAGTCTTCAACGCTGTG 360  
Db 301 TCCTGCTTACAGTATTTGCTCTTATTTAGTACGATCCAGTCAAGTCTTCAACGCTGTG 360

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Db 301 TCTGTATATAACATTGCTCTCATCAGCTATGATCGATACCTGTGCTCAAAATGCTGTG 360
Qy 361 CGTTATAGACACACACACTGGCATCTGAAATTTGTTGCTCAAAATGGTGGCTGTTGG 420
Db 361 TCTTATAGAACTCAACATACCTGGGCTCTTGAAGATTTGTTACTCTGATGGTGGTGGTGG 420
Qy 421 ATACTGGCTTTCTTGGTCAATGGCCCAATGATTTGCTGGCTTCGGATTTCTTGGAAAGACAGC 480
Db 421 GTGCTGGCTTCTTGTAGTGAATGGGCCAATGATTTCTAGTTTTCAGAGTCTTGGGAAGA--- 476
Qy 481 ACCAACACAGAGGAGTGGAGCTGGCTTTCTTACTGAGTGGTACATCCTCGCCATTACA 540
Db 477 --TGAAGGTAGTGAATGTAACCTGGATTTTTTTCGGAATGGTACATCCTTGGCCATACA 534
Qy 541 GCATTTCTTGGAAATTCCTGCTCCCTGCTCTCTTGGTGGTCTATTTTCAGTGTACAGATTTAC 600
Db 535 TCATTTCTTGGAAATTCGTTAGTCCCACTCATCTTAGTCTGCTTATTTTCAACATGAATTTAT 594
Qy 601 TGGAGCTGTGGAAGCTGGAGTCTCAGTAGTGGCTTAGCCCTAGCCAGCTGGATTCATCGCT 660
Db 595 TGGAGCTGTGGAAGCTGGAGTCTCAGTAGTGGCTTAGCCCAAGCCATCCTGGACTGACTGCT 654
Qy 661 ACCTTTCCAGGGGCACTGGACACTCAGCAGACTGGTGGCTTGTAGACAAAGTCTT 720
Db 655 GTCTTTCCAACTCTGTGGACACTCATTCAGAGTAGACTATCTTCAAGGAGATCTCTT 714
Qy 721 CCTGGATTAAAGGAACAGCGCCATCCTTCATTCAGAAAGTCCACAGGAGAAAGAGAGT 780
Db 715 TCTGATCGACAGAAAGTTCTGTCATCTTTCATTCAGAGAGCGGAGGAGAGAGTAGT 774
Qy 781 CTCCTGTGTCTTAAAGACTCAGATGAGCGGTAGTATCATCGCTTCAAAGTGGGTTC 840
Db 775 CTCATGTTTTCTCAAGAACCAAGATGAATAGCAATACAATTTGCTTCCAAAATGGTTC 834
Qy 841 TTCTCGCGATCAGAAAGCCAGTCTTCCAGAGAGAGCAGCTGGAGCTTCTCAGAGGC 900
Db 835 TTCTCCCAATCAGATTTCTGTAGCTTTCACCAAGGGAACATGTTGAACCTCTTAGAGCC 894
Qy 901 AGAAGCTAGCCAGTGGCTAGTGTCTCTCTGAGTGTCTTTTGCCATTTGCTGGGCTCCG 960
Db 895 AGGAGATTAGCAAGTCACTGGCCATCTCTTAGGGGTTTTGCTGTTGCTGGGCTCCA 954
Qy 961 TATTGCTGTTCACAAATGCTTTTCAACTTATCGCAGAGGGGAGCGCCCAATCGATT 1020
Db 955 TATTCTGTGTCAAAATGCTTTTCACTTTTATTTCTCAGCAACAGGCTCTTAATCAGTT 1014
Qy 1021 TGTACAGCATAGCTTTTGGCTACAGTGGTTCATTTCACTTATTAATCCCTTCTATAC 1080
Db 1015 TGGTATAGAAATGCAATTTTGGCTTCAGTGGTTCATTTCTTTGTCAATCTCTTTTGTAT 1074
Qy 1081 CCTTTGTGCCACAGACGTTTCCAGAGGCTTTCTGGAAGATACCTCTGTGTGACAAAGCAA 1140
Db 1075 CCATTGTGTCAAGCGCTTTCAAAGGCTTTCTTGAAATATTTTGTATATAAAGAAAGCAA 1134
Qy 1141 CAGACCTTTC---ACAGACCCAGTCAATGATTTCTTTGA 1176
Db 1135 CCTCTACCACACAAACAGTGGCTGAGTATCTTCTTAA 1173
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## RESULT 13

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US-10-272-983-13
; Sequence 13, Application US/10272983
; Publication No. US20030148450A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Dang, Huong T.
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
; FILE REFERENCE: AREN0050
; CURRENT APPLICATION NUMBER: US/10/272,983
; CURRENT FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: US/09/417,044
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; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 60/109,213
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,851
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/123,946
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,949
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/136,436
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,437
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,439
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,567
; PRIOR FILING DATE: 1999-05-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-272-983-13
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Query Match 56.9%; Score 669; DB 15; Length 1173;
Best Local Similarity 74.2%; Pred. No. 1.7e-202;
Matches 875; Conservative 0; Mismatches 295; Indels 9; Gaps 2;

Qy 1 ATGTCGGAGTCTAACGGCACTGACGCTGTGCGCACTGCTCAAGTCCCTTGGCATTTT 60
Db 1 ATCCGATACATAATAGCAACAATTAATCATCTAGCACTCGTGTACTTTAGCATTT 60
Qy 61 TTAATGTCCTGCTGCTTTTGTCTATAACGATAGGCAATGCTGTGGTCAATTTAGCCCTT 120
Db 61 TTTATGTCCTTAGTAGCTTTTGTCTATAATGCTAGGAAATGCTTTGGTCAATTTAGCTTT 120
Qy 121 GTACGACAGAAACCTTAGACATCGAAGTAATTTTCTTAATTTGGCTATTTCT 180
Db 121 GTGGTGACAAAAACCTTAGACATCGAAGTAGTTATTTTCTTAATTTGGCCATCTCT 180
Qy 181 GACTTCTTCTGGGTGTCTCATCTCCATTCCTCTGTACATCCCTCACAGCTGTTTAACTGG 240
Db 181 GACTTCTTCTGGGTGTCTCATCTCCATTCCTTGTACATCCCTCACAGCTGTTTAACTGG 240
Qy 241 AATTTTGGAAAGTGAATCTGCATGTTTTGGCTCAATTAATGCTATCTTTTGTGACACAGCA 300
Db 241 GATTTTGGAAAGGAAATCTGTGATTTTGGCTCACTACTGACTATCTGTTATGTACAGCA 300
Qy 301 TCGTCTACAGTATTTGCTCCTCATTTAGCTACGATCGATACCAGTTCAGTTTCAAAAGCTGTG 360
Db 301 TCTGTATATAACATTTGCTCCTCATCAGCTATGATCGATACCTGTGCTCAGTCTCAATGCTGTG 360
Qy 361 CGTTATAGACACAGCACACTGGCATCTGGAATTTGTTACTGAGTGGTACATCCTCGCCATTACA 420
Db 361 TCTTATAGAACTCAACATACCTGGGCTCTTGAAGATTTGTTACTCTGATGGTGGCCGCTTGG 420
Qy 421 ATACTGGCTTTCTTGGTCAATGGCCCAATGATTTCTGCTGCTGGATTTCTTGGAAAGAACAGC 480
Db 421 GTGCTGGCTTCTTGTAGTGAATGGCCCAATGATTTCTAGTTTTCAGAGTCTTGGGAAGA--- 476
Qy 481 ACCAACACAGAGGAGTGGAGCTGGCTTTGTTACTGAGTGGTACATCCTCGCCATTACA 540
Db 477 --TGAAGGTAGTGAATGTAACCTGGATTTTTTTCGGAATGGTACATCCTTGGCCATACA 534
Qy 541 GCATTTCTTGGAAATTCCTGCTCCCTGCTCTCTTGGTGGTCTATTTTTCAGTGTACAGATTTAC 600
Db 535 TCATTTCTTGGAAATTCGATGATCCAGTCACTCTTAGTCTGCTTATTTTCAACATGAATTTAT 594
Qy 601 TGGAGCTGTGGAAGCTGGAGTCTCAGTAGTGGCTTAGCCCTAGCCAGCTGGATTCATCGCT 660
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Db 595 TGGAGCTGTGGAAGCGTGATCATCTCAGTAGTGGCAAGCCATCTCTGGACTGACTGCT 654
Qy 661 ACCTCTTCAGAGGCGACTGAGACACTCAGCGAGAACTGGGTGGCTGTAGGACAAAGTCTT 720
Db 655 GTCTCTTCCAACATCTGTGACACTCATCTCAGAGGTAGACTATCTTCAAGGAGATCTCTT 714
Qy 721 CTTGGATTAAAGGAACAGCGCGATCCCTTCATTCAGAGAGTCCAGAGGAAAGAGCAGT 780
Db 715 TCTGCAATCGACAGAGTTCCTGATCTCTTCAATTCAGAGAGAGAGAGAGAGTAGT 774
Qy 781 CTCTGCTGTCTTAAGGACTCACATGAGCGGTAGTAGTATCATCGCTTCAAAGTGGGTTC 840
Db 775 CTCATGTTTTCTCAAGAACCAAGATGAATAGCAATTAATGCTTCCAAAGTGGGTTC 834
Qy 841 TTCTGCGGATCAGAAAGCCAGTGTCTTACCAGAGAGAGACAGTGGAGCTTCTCAGAGGC 900
Db 835 TTCTCCCAATCAGATTCTGTAGCTCTTCAACAAAGGGAACATGTTGAACCTGCTTAGAGCC 894
Qy 901 AGAAGCTAGCCAGGTGCTAGTCTCTCTGAGTGTCTTTGCCATTTTGGCTGGCTCCG 960
Db 895 AGAGATTAGCCAAAGTCACTGGGCATCTCTTAGGGGTTTTTGTCTGTCTGGGCTCCA 954
Qy 961 TATTGCTGTTCACAAATGTTCTTCAACTTATCGCAGAGGGAGCGGCCCAAAATCGATT 1020
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Db 1015 TGGTATAGAAATTCATTTTGGCTTCAAGTGTTCATTTCTTGTCAATCTCTTTGTAT 1074
Qy 1081 CCTTTGGCCACAGAGCTTTCCAGAGGCTTTCTGGAAGATCTCTGTGTGACAAAGCAA 1140
Db 1075 CCATTGTGTCACAGGCGCTTCAAAAGGCTTCTTGAAATATTTTGTATAAAAGCAA 1134
Qy 1141 CCAGCACCTTC---ACAGACCCAGTCTCAGTATCTTCTTGA 1176
Db 1135 CCTTACCATCACACACAGTCTGGTCAATCTTCTTAA 1173
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## RESULT 14

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US-10-354-769-1
; Sequence 1, Application US/10354769
; Publication No. US20030149242A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer Inc.
; APPLICANT: O'Reilly, Mark A.
; APPLICANT: Peter, Beate
; TITLE OF INVENTION: NOVEL POLYPEPTIDE
; FILE REFERENCE: PC10373B
; CURRENT APPLICATION NUMBER: US/10/354,769
; CURRENT FILING DATE: 2003-01-30
; PRIOR APPLICATION NUMBER: US 09/698,801
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/211,243
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: GB 9925641.4
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: GB 0009973.9
; PRIOR FILING DATE: 2000-04-20
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-354-769-1
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Query Match 56.98; Score 669; DB 15; Length 1173;
Best Local Similarity 74.2; Pred. No. 1.7e-202;
Matches 875; Conservative 0; Mismatches 295; Indels 9; Gaps 2;
Qy 1 ATGTGCGAGTCTAAAGCGCACTGAGCTCTTGCCACTGCTCTCAAGTCCCGCTTGGCATTT 60
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Qy 421 ATACTGGCTTTCTTGTGTCATGATGCCCAATGATTTCTGGCTTTCGATTTCTTGGAAAGACAGC 480
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Db 775 CTCATGTTTTCTTCAAGAAACCAAGATGAATAGCAATTAATTTCTTCCAAAGTGGGTTC 834
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Db 835 TTCTCCCAATCAGATTCTGTAGCTCTTCAACAAAGGGAACATGTTGAACCTGTTAGAGCC 894
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Db 1135 CCTCTACCATCAACAACAGTCGGTCAGTATCTTCTTAA 1173

## RESULT 15

US-10-393-807-13  
; Sequence 13, Application US/10393807  
; Publication No. US20030175891A1  
; GENERAL INFORMATION:  
; APPLICANT: Chen, Ruoping  
; APPLICANT: Dang, Huong T.  
; APPLICANT: Liaw, Chuen W.  
; APPLICANT: Lin, I-Lin  
; TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors  
; FILE REFERENCE: AREN0050  
; CURRENT APPLICATION NUMBER: US/10/393,807  
; CURRENT FILING DATE: 2003-03-21  
; PRIOR APPLICATION NUMBER: US/09/417,044  
; PRIOR FILING DATE: 1999-10-12  
; PRIOR APPLICATION NUMBER: 60/109,213  
; PRIOR FILING DATE: 1998-11-20  
; PRIOR APPLICATION NUMBER: 60/120,416  
; PRIOR FILING DATE: 1999-02-16  
; PRIOR APPLICATION NUMBER: 60/121,851  
; PRIOR FILING DATE: 1999-02-26  
; PRIOR APPLICATION NUMBER: 60/123,946  
; PRIOR FILING DATE: 1999-03-12  
; PRIOR APPLICATION NUMBER: 60/123,949  
; PRIOR FILING DATE: 1999-03-12  
; PRIOR APPLICATION NUMBER: 60/136,436  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/136,437  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/136,439  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/136,567  
; PRIOR FILING DATE: 1999-05-28  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 74  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 13  
; LENGTH: 1173  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-393-807-13

Query Match 56.9%; Score 669; DB 16; Length 1173;  
Best Local Similarity 74.2%; Pred. No. 1.7e-202;  
Matches 875; Conservative 0; Mismatches 295; Indels 9; Gaps 2;  
Qy 1 ATGTCGGAGTCTAACGGCACTGACGCTCTTGGCACTGCTCAAGTCCCTTGGCAATTT 60  
Db 1 ATGCCAGATATAATAGCACAACTAATTTATCAATGCACTCTCGTGTACTTTAGCAATTT 60  
Qy 61 TTAATGTCCTTGGCTGCTTTTGGCTATAACGATAGGCAATGCTGTGCTCATTTTAGCCCTTT 120  
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Search completed: August 5, 2005, 15:08:29  
Job time : 781 secs

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Db 361 TCTTATAGAACTCAACATACCTGGGGCTTGAAGATTTGTTACTCTGTGATGGTGGCCGCTTTGG 420  
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Db 421 GTGCTGGCTTTCTTTAGTGAATGGGCCAATGATTTCTAGTTTCAGAGTCTTTGGAAAGCA--- 476  
Qy 481 ACCAACACAGAGGAGTGGGAGCTGGCTTTGTTTACTAGTGGTACATCCTCGCCATTTACA 540  
Db 477 --TGAAGGTAGTGAATGTGAACCTGGATTTTTTTTGGAAATGGTACATCCTTTGCCATCACA 534  
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Db 535 TCATTTTGGAAATTCGTGATCCAGTCTATCTTAGTCTGCTTATTTTCAACATGAATATTTAT 594  
Qy 601 TGGAGCCTGTGGAAGCGTGGAGTCTCAGTAGGTGCTCCTAGCCAGCTGGATTTTCACTCGCT 660  
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Db 835 TTCTCCCAATCAGATTTCTGTAGCTCTTCCAAAGGGAACATGTTGAACCTGCTTAGAGCC 894  
Qy 901 AGGAAGCTAGCCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960  
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Db 1075 CCATTTGTCAACAGCGCTTTTCAAAAGGCTTTCTTGAAGATATTTTGTATATAAAAGCAA 1134  
Qy 1141 CCAGCACCTTC---ACAGACCAGTCAGTATCTTCTTGA 1176  
Db 1135 CCTCTACCATCAACAACAGTCGGTCAGTATCTTCTTAA 1173

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

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Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: geneseqn1990s.\*  
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5: geneseqn2001bs.\*  
6: geneseqn2002as.\*  
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11: geneseqn2003ds.\*  
12: geneseqn2004as.\*  
13: geneseqn2004bs.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1176	100.0	1176	6	Aai70982 Rat hist
2	958.4	81.5	1176	6	Aai70981 Mouse his
3	958.4	81.5	1538	12	Ado30257 Mouse GPC
4	670.6	57.0	1173	6	Aai67750 Human his
5	669	56.9	1173	3	Aaa46023 Human G p
6	669	56.9	1173	3	Aad01124 Human G p
7	669	56.9	1173	3	Aaf83203 Human GPC
8	669	56.9	1173	5	Aah24007 Human G p
9	669	56.9	1173	6	Abz80663 Human his
10	669	56.9	1173	6	Abq78739 Nucleotid
11	669	56.9	1173	6	Aai70980 Human his
12	669	56.9	1173	8	ACA93262 Human cDN
13	669	56.9	1173	10	Adg98759 Human GPC
14	669	56.9	1173	10	Abz57063 Human cDN
15	669	56.9	1173	11	Adj26922 Human end
16	669	56.9	1173	12	ADG86374 Human end
17	669	56.9	1173	12	ADJ88375 Novel hum
18	669	56.9	1173	12	ADP20167 Human G p
19	669	56.9	1173	12	ADQ75073 Human cDN
20	669	56.9	1227	4	Aai66009 Human GPR

21	669	56.9	1265	6	Aas98078 Human DNA
22	669	56.9	1265	9	Aad55125 Human H4
23	669	56.9	1266	6	Abk12959 DNA seque
24	669	56.9	1300	6	ABA02496 Human G p
25	669	56.9	1312	4	Aah47911 Human G p
26	669	56.9	3689	8	Abz42573 Human his
27	669	56.9	3689	12	Ado05719 Human his
28	669	56.9	3689	12	Ado29967 Human GPC
29	668	56.8	1170	9	Aad55126 Human H4
30	616.8	52.4	1170	6	Aai70983 Guinea pi
31	494.6	42.1	1166	9	Aad55124 Human H4
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33	288.4	22.8	1326	6	Aad37667 Human G-p
34	257.8	21.9	540	6	Aas98150 Human DNA
35	158.4	13.5	1239	2	AAx84570 G-protein
36	158.4	13.5	1239	3	AAx70639 Rat G-pro
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41	140.6	12.0	1338	12	ADf66834 Murine hi
42	140.6	12.0	18105	8	Abz82337 Mouse his
43	140	11.9	1098	4	AAH47749 Human his
44	139	11.8	2483	12	Ado30256 Mouse GPC
45	138.4	11.8	1023	4	AAH26798 Human his

## ALIGNMENTS

RESULT 1  
AAI70982  
ID AAI70982 standard; cDNA; 1176 BP.  
XX  
AC AAI70982;  
XX  
DT 18-MAR-2002 (first entry)  
XX  
DE Rat histamine H4 receptor cDNA.  
XX  
KW Histamine H4 receptor; rat; antiaesthetic; antiallergenic;  
KW antiinflammatory; cardiant; circulatory; antidiabetic; laxative;  
KW diagnosis; gene therapy; ss.  
XX  
OS Rattus rattus.  
XX  
PN WO200192485-A1.  
XX  
PD 06-DEC-2001.  
XX  
PF 22-FEB-2001; 2001WO-US005914.  
XX  
PR 31-MAY-2000; 2000US-0208260P.  
XX  
PA (ORTH ) ORTHO-MCNEIL PHARM INC.  
XX  
PI Lovenberg T, Liu C;  
XX  
DR WPI; 2002-114339/15.  
XX  
DR P-PSDB; AAM50566.  
XX  
PT New mammalian histamine H4 receptor proteins and polynucleotides encoding  
PT the proteins, useful in gene therapy for treating diseases where it is  
PT beneficial to elevate mammalian histamine H4 receptor activity.  
XX  
PS Claim 4; Fig 5C; 92pp; English.  
XX  
CC The present sequence is that of a cDNA clone encoding a rat histamine  
CC receptor of the H4 subtype. The cDNA was isolated from a rat spleen cDNA  
CC library. It shows 72.5% homology to the human H4 receptor coding region.  
CC The invention provides mammalian (human, mouse, rat and guinea pig)  
CC histamine H4 receptor nucleic acid molecules (see AAI70980-83) and  
CC polypeptides (see AAM50564-67). The nucleic acids have been expressed in



CC recombinant host cells that produce active recombinant protein. The  
 CC pharmacology of known histamine ligands is demonstrated. Mammalian  
 CC histamine H4 receptor may be used in gene therapy for the treatment of  
 CC diseases where it is beneficial to elevate mammalian histamine H4  
 CC receptor activity. Recombinant protein is useful for identifying  
 CC modulators of the mammalian histamine H4 receptor. Such modulators may be  
 CC useful for diagnosing, treating or preventing asthma, allergy,  
 CC inflammation, cardiovascular and cerebrovascular disorders, non-insulin  
 CC dependent diabetes mellitus, hyperglycemia, constipation, arrhythmia,  
 CC disorders of the neuroendocrine system, stress and spasticity  
 XX  
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 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1176; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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 Db 361 CGTTATAGACACAGCACACCTGGCATCTGAAATTTGTTGCTCAATGGTGGCTGTTGG 420  
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 Db 841 TTCTGCGATCAGAAAGCCAGTCTTACCAGAGAGACACGTGGAGCTTCTCAGAGGC 900  
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 ID AAI70981 standard, cDNA; 1176 BP.  
 XX  
 AC AAI70981;  
 XX  
 DT 18-MAR-2002 (first entry)  
 XX  
 DE Mouse histamine H4 receptor cDNA.  
 XX  
 KW Histamine H4 receptor; mouse; antiasthmatic; antiallergenic;  
 KW antiinflammatory; cardiant; circulatory; antidiabetic; laxative;  
 KW diagnosis; gene therapy; ss.  
 XX  
 OS Mus musculus.  
 XX  
 PN W0200192485-A1.  
 XX  
 PD 06-DEC-2001.  
 XX  
 PF 22-FEB-2001; 2001WO-US005914.  
 XX  
 PR 31-MAY-2000; 2000US-0208260P.  
 XX  
 PA (ORTH ) ORTHO-MCNEIL PHARM INC.  
 XX  
 PI Lovenberg T, Liu C;  
 XX  
 DR WPI; 2002-114339/15.  
 DR P-PSDB; AAM50565.  
 XX  
 PT New mammalian histamine H4 receptor proteins and polynucleotides encoding  
 PT the proteins, useful in gene therapy for treating diseases where it is  
 PT beneficial to elevate mammalian histamine H4 receptor activity.  
 XX  
 PS Claim 4; Fig 5A; 92pp; English.  
 XX  
 CC The present sequence is that of a cDNA clone encoding a murine histamine  
 CC receptor of the H4 subtype. The cDNA was isolated from a mouse spleen  
 CC cDNA library. It shows 72.8% homology to the human H4 receptor coding  
 CC region. The invention provides mammalian (human, mouse, rat and guinea  
 CC pig) histamine H4 receptor nucleic acid molecules (see AAI70980-83) and  
 CC polypeptides (see AAM50564-67). The nucleic acids have been expressed in  
 CC recombinant host cells that produce active recombinant protein. The  
 CC pharmacology of known histamine ligands is demonstrated. Mammalian  
 CC histamine H4 receptor may be used in gene therapy for the treatment of  
 CC diseases where it is beneficial to elevate mammalian histamine H4  
 CC receptor activity. Recombinant protein is useful for identifying



CC modulators of the mammalian histamine H4 receptor. Such modulators may be  
CC useful for diagnosing, treating or preventing asthma, allergy,  
CC inflammation, cardiovascular and cerebrovascular disorders, non-insulin  
CC dependent diabetes mellitus, hyperglycemia, constipation, arrhythmia,  
CC disorders of the neuroendocrine system, stress and spasticity  
XX  
SQ Sequence 1176 BP; 263 A; 281 C; 269 G; 363 T; 0 U; 0 Other;

Query Match 81.5%; Score 958.4; DB 6; Length 1176;  
Best Local Similarity 88.4%; Pred. No. 2.9e-300;  
Matches 1040; Conservative 0; Mismatches 136; Indels 0; Gaps 0;

Qy 1 ATGTCGAGTCTAACGGCACTGAGCTCTTGCCACTGACTGCTCAAGTCCCTTGSCATTT 60  
Db 1 ATGTCGAGTCTAACAGTACTGGCATCTTGCCACAGCTGCTCAGTCCCTTGSCATTT 60  
Qy 61 TTAATGTCCTTGTCTTTGCTATACGATAGGCAATGCTGTGGTCATTTTAGCCCTTT 120  
Db 61 TTAATGTCCTTGTCTTTGCTATATATGATAGGCAATGCTGTGGTCATTTTAGCCCTTT 120  
Qy 121 GTAGCAGAGAAACCTTAGACATCGAAGTAATATTTTCTTAATTTGGCTATTTCT 180  
Db 121 GTGTGGACAGAAACCTTAGACATCGAAGTAATATTTTCTTAATTTGGCTATTTCT 180  
Qy 181 GACTTCTCGTGGTGTCTATCCATTCCTCTGTACATCCCTCACACGCTGTTAACTGG 240  
Db 181 GACTTCTCGTGGTGTCTATTTCCATTCCTCTGTACATCCCTCACACGCTGTTAACTGG 240  
Qy 241 AATTTGGAAGTGGAAATCGCATGTTTGGCTCATTTACTGACTATCTTTTGTGCACACA 300  
Db 241 AATTTGGAAGTGGAAATCGCATGTTTGGCTCATTTACTGACTATCTTTTGTGCACACA 300  
Qy 301 TCCGCTACAGTATGTCCTCATTAGTACGATCGATACCATGATGTTTCAACGCTGTG 360  
Db 301 TCTGTCTACAATATGTCCTCATTAGTACGATCGATACCATGATGTTTCAACGCTGTG 360  
Qy 361 CGTTATAGACACAGCAGTGGCATCTGAAATTTGCTCAAAATGGTGGCTGTTTGG 420  
Db 361 TCATTATAGGCTCAACACACTGGCATCATGAAGATTTGTTCAAAATGGTGGCTGTTTGG 420  
Qy 421 ATACTGGCTTTTGGTCAATGGCCCAATGTTCTGGCTTCGGATCTTGGAAAGAACAGC 480  
Db 421 ATACTGGCTTTTGGTCAATGGCCCAATGTTCTGGCTTCGGATCTTGGAAAGAACAGC 480  
Qy 481 ACCAACACAGAGGAGTGGAGCTGGCTTTGTTACTGAGTGGTACATCTCCGCCATTACA 540  
Db 481 ACRAACACAAAGGACTGTGAGCTGGCTTTGTTACAGAGTGTACATCTCCACCAATTACA 540  
Qy 541 GCATCTTTGGAAATTCCTGCTCCCTGCTCTCCTGGTGGTCTATTTCAAGTGTACAGATTAC 600  
Db 541 ATGCTCTTTGGAAATTCCTGCTCCCTGCTCTCCTGGTGGTCTATTTCAATGTACAGATTAC 600  
Qy 601 TGGAGCTGTGGAAGCTGGAGTCTCAGTAGGTGCTCCTAGTGGCTGGATTCATGCT 660  
Db 601 TGGAGCTGTGGAAGCTGGAGTCTCAGTAGGTGCTCCTAGTGGCTGGATTCATGCT 660  
Qy 661 ACCTCTTCCAGGGCACTGGACACTCAGCAGAACTGGGTTGGCTTTGAGACAGTCTT 720  
Db 661 ACCTCTTCCAGGTCTTCCAGCACCTTACAGAGCTGGGTTGGCTTTGAGACAGTAAAT 720  
Qy 721 CCTGATTAAAGGAACAGCGGCTATCCCTTCAATTCAGAAAGTCCACAGGAAAGAGAGT 780  
Db 721 CCTGATTAAAGGAATCAGTGCATCTCGTCACTCAGAAAGTCCCTCAGAAAGAGAGCAGC 780  
Qy 781 CTCCTGGTGTCTTAAGGACTCACATGAGCGGTAGTATCATCGCTTCAAGTGGGTTCC 840  
Db 781 ATCTGGTGTCTTAAAGGACTCACATGAGCGGTAGTATCATCGCTTCAAGTGGGTTCC 840  
Qy 841 TTCTCCGATCAGAAAGCCAGTCTTCCACAGAGAGCAGTGGAGCTTCTCAGAGGC 900  
Db 841 TTCTGGCATCGAAAGTGCAGGCTTTCGCCAAGGGAGTACGCAGAGCTTCTCAGAGGC 900  
Qy 901 AGGAAGCTAGCAGGCTAGTCTGCTCTGCTAGTGTCTTTTGGCAATTTGCTGGGCTCCG 960

Db 901 AGGAAGCTAGCAGGCTAGTCTGCTCTGAGCGCTTTTGGCAATTTGCTGGGCTCCA 960  
Qy 961 TATTGCTGTTTCAACAATTTGTTTCAACTTATCGAGAGGAGCGCCCAAAATCGATT 1020  
Db 961 TACTGTCTGTTTCAACAATTTGTTTCAACTTATCGAGAGGAGCGCCCAAAATCGG 1020  
Qy 1021 TGGTACAGATAGCTTTTGGCTACAGTGGTTCAAATCACTATTAATCCCTTCTATAC 1080  
Db 1021 TGGTACAGATAGCTTTTGGCTACAGTGGTTCAAATCGTTTGTAAATCCCTTCTGTAC 1080  
Qy 1081 CCTTTGTGCCACAGACGTTTCCAGAGGCTTCTCGGAAGATCTCTGTGTGACAAAGCAA 1140  
Db 1081 CCTTTGTGCCACAGGCTTTCAGAGGCTTCTCGGAAGATCTCTGTGTGACAAAGCAA 1140  
Qy 1141 CCAGCAGCTTCCAGAGACCCAGTCAATGATCTTCTTGA 1176  
Db 1141 CCAGCGCTGTCCAGAGAACCCAGTCAATGATCTTCTTGA 1176  
RESULT 3  
ADO30257  
ID ADO30257 standard; cDNA; 1538 BP.  
XX  
AC ADO30257;  
XX  
DT 29-JUL-2004 (first entry)  
XX  
DE Mouse GPCR HRH4 polynucleotide, SEQ ID NO:1360.  
KW G protein-coupled receptor; GPCR; drug screening; diagnosis;  
KW transgenic mouse; neurological disorder; adrenal gland disorder;  
KW colon disorder; intestinal disorder; cardiovascular disorder;  
KW muscular disorder; blood disorder; immune disorder; bone disorder;  
KW joint disorder; metabolic disorder; nutritive disorder; cancer;  
KW kidney disorder; liver disorder; lung disorder; breast disorder;  
KW ovary disorder; uterus disorder; prostate disorder; testis disorder;  
KW skin disorder; stomach disorder; pancreas disorder; spleen disorder;  
KW thymus disorder; thyroid disorder; antiparkinsonian; antimanic;  
KW cytosolic; antinflammatory; vasotropic; antidiarrhoeic; antiarrhythmic;  
KW CNS; central nervous system; respiratory; antidiarrhoeic; antidiabetic;  
KW virucide; hepatotropic; antibacterial; antianaemic; antiseborrhoeic;  
KW dermatological; antiulcer; antithyroid; antiallergic; anorectic;  
KW immunosuppressive; nephrotropic; gene therapy; GPCR modulator; mouse;  
KW murine; gene; ss.  
XX  
OS Mus musculus.  
XX  
WO2004040000-A2.  
XX  
PD 13-MAY-2004.  
XX  
PF 09-SEP-2003; 2003WO-US028226.  
XX  
PR 09-SEP-2002; 2002US-0409303P.  
PR 09-APR-2003; 2003US-0461329P.  
XX  
PA (PRIM-) PRIMAL INC.  
XX  
PI Gaitanaris GA, Bergmann JE, Gragerov A, Hohmann J, Li F;  
PI Madisen L, McIlwain KL, Pavlova MN, Vassilatis D, Zeng H;  
XX  
DR WPI; 2004-390329/36.  
DR P-PSDB; ADO29497.  
XX  
PT Novel mammalian G protein coupled receptors, useful for identifying  
PT compounds that modulates diagnosing and treating disease condition  
PT associated with GPCR dysfunction e.g. autoimmune diseases, angina  
PT pectoris, Parkinson's disease.  
XX  
PS Claim 151; SEQ ID NO 1360; 542pp; English.  
XX  
CC The invention relates to human and mouse G protein-coupled receptors

CC (GPCRs) and nucleic acids encoding them. The invention also relates to  
CC sequences at least 90% identical to the GPCR proteins and nucleic acids  
CC of the invention; methods of treating, preventing or diagnosing diseases  
CC associated with GPCRs of the invention; methods of screening for  
CC compounds useful in the treatment of GPCR-related diseases; a transgenic  
CC mouse comprising a GPCR gene of the invention; a mouse comprising a  
CC mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived  
CC from the transgenic mice; kits comprising several mice, each of which has  
CC a mutation in a different GPCR gene of the invention; and kits comprising  
CC probes which hybridize to GPCR polynucleotides of the invention. The  
CC invention further discloses variants of the GPCR polypeptides and vectors  
CC comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may  
CC be used in the diagnosis, treatment or prevention of a wide variety of  
CC diseases including neurological disorders (e.g., Alzheimer's disease,  
CC depression, diabetic neuropathy, Parkinson's disease or schizophrenia);  
CC disorders of the adrenal gland; disorders of the colon or intestine  
CC (e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel  
CC syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or  
CC myocardial infarction); muscular disorders; blood disorders (e.g.,  
CC anaemia or leukaemia); immune disorders (e.g., autoimmune disorders or  
CC AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid  
CC arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g.,  
CC obesity, enzyme deficiency-related diseases or vitamin deficiency-related  
CC diseases); and disorders of the kidney, liver, lung, breast, ovary,  
CC uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and  
CC thyroid (e.g., cancers). The present sequence represents a GPCR-encoding  
CC nucleic acid of the invention. Note: The full sequence data for this  
CC patent did not form part of the printed specification; those sequences  
CC not shown were obtained in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 1538 BP; 357 A; 362 G; 340 C; 479 T; 0 U; 0 Other;

Query Match 81.5%; Score 958.4; DB 12; Length 1538;  
Best Local Similarity 88.4%; Pred. No. 3.4e-300;  
Matches 1040; Conservative 0; Mismatches 136; Indels 0; Gaps 0;  
QY 1 ATGTCGGAGCTAAGCGACCTGAGCTCTGCGACCTGCTCAAGTCCCTCGCATTT 60  
DB 61 ATGTCGGAGCTAAGCGACCTGAGCTCTGCGACCTGCTCAAGTCCCTCGCATTT 120  
QY 61 TTAATGTCCTTCATTTGCTTTGCTATAACGATAGGCAATGCTGTGCTATTTAGCCCTTT 120  
DB 121 TTAATGTCCTTCATTTGCTTTGCTATAACGATAGGCAATGCTGTGCTATTTAGCCCTTT 180  
QY 121 GTACACAGACAAACCTTAGACATCGAAGTAATTTATTTTCTTAATTTGGCTATTCT 180  
DB 181 GTGCTGGACAGAAACCTTAGACATCGAAGTAATTTATTTTCTTAATTTGGCTATTCT 240  
QY 181 GACTTCTTCGTGGGTGTCATCTCCATTCCTGTACATCCCTCACAGCTGTTTAACTGG 240  
DB 241 GACTTCTTCGTGGGTGTCATCTCCATTCCTGTACATCCCTCACAGCTGTTTAACTGG 300  
QY 241 AATTTGGAAGTGAATCTGCATGCTTTTGGCTCATTACTGACTATCTTTTGTGCACAGCA 300  
DB 301 AATTTGGAAGTGAATCTGCATGCTTTTGGCTCATTACTGACTATCTTTTGTGCACAGCA 360  
QY 301 TCCGTCTACAGTATTGCTCCTCATTTAGCTACGATCGATACAGTCAAGTTTCAACCGCTGTG 360  
DB 361 TCTGTCTACAAATATTGCTCCTATTAGCTACGATCGATACAGTCAAGTTTCAACCGCTGTG 420  
QY 361 CGTTTATAGACACAGCACCTGGGATCTGGAATTTGTTGCTCAAAATGGTGGCTGTTGG 420  
DB 421 TCTTATAGGGCTCAACACCTGGGATCATGAAGATTTGTTGCTCAAAATGGTGGCTGTTGG 480  
QY 421 ATACTGGCTTTCTTTGGTCAATGGCCCAATGATTTCTGGCTTCGGATTTCTTGAAGAAGCAGC 480  
DB 481 ATACTGGCTTTCTTTGGTCAATGGCCCAATGATTTCTGGCTTCGGATTTCTTGAAGAAGCAGC 540  
QY 481 ACCAACACAGAGGAGTGGAGCTGGCTTTGTTTACTGAGTGGTACATCTCGCCATTACA 540  
DB 541 ACGAACACAAAGGAGCTGTGAGCCCTGGCTTTGTTTACAGAGTGGTACATCTCCACCATACA 600

QY 541 GCATTCTTGGAAATCTCTGCTCCCTGCTCTCTGCTGCTATTTTCAAGTGTACAGATTATAC 600  
DB 601 ATGCTCTTGGAAATCTCTGCTCTCTGCTCTCTGCTCATCTCTGCTGCTTATTTCAATGTACAGATTATAC 660  
QY 601 TGGAGCTCTTGGAAAGCGTGGAGTCTCTCAGTGTGCTTGTAGCCACGCTTGAATTCATCGCT 660  
DB 661 TGGAGCTCTTGGAAAGCGTGGAGTCTCTCAGTGTGCTTGTAGCCACGCTTGTGATTTCTCCACT 720  
QY 661 ACCTCTCCAGGGGCACTGGACACTCACGAGAACTGGGTGGCTTGTAGGACAAGTCTT 720  
DB 721 ACCTCTTCCAGTCTCTCAGGACACTTACACAGAGCTGGGTGGCTTGTAGGACAAGTCTT 780  
QY 721 CTTGGATTAAAGGAAACAGCGCGCATCCCTTCAATTCAGAAAGTCCACGAGAAAGAGCAGT 780  
DB 781 CTTGGATTAAAGGAAACAGCTGCTCTCTCAGTGTGCTTGTAGGACAAGTCTCTCGAAGAAAGAGCAGC 840  
QY 781 CTCTGTGTCTTAAAGGACTCATGAGCGGTAGTATCATCGCTTCAAAAGTGGGTCTC 840  
DB 841 ATCTGTGTCTTAAAGGACTCATGAGCGGTAGTATCATCGCTTCAAAAGTGGGTCTC 900  
QY 841 TTCTGCGGATCAGAAAGCCAGTCTTCCACGAGAGAGCAGTGGAGCTTCTCAGAGGC 900  
DB 901 TTCTGCGGATCAGAAAGTGGAGCTTCCGCAAGGAGTACGAGAGCTTCTCAGAGGC 960  
QY 901 AGGAAGCTAGCCAGGTGCTGTCTCTGAGTGTCTCTGAGTGTCTTTTGGCATTTTGTGGCTCCG 960  
DB 961 AGGAAGCTAGCCAGGTGCTGTCTCTGAGTGTCTCTGAGTGTCTTTTGGCATTTTGTGGCTCCA 1020  
QY 961 TATTGCTGTTCACAAATTTGTTTCAACTTATTCGAGAGGGAGCGCCCAATTCGATT 1020  
DB 1021 TACTGTCTGTTCACAAATTTGTTTCAACTTATTCGAGTGTCTCTGAGTGTCTTTTGGCATTTTGTGGCTG 1080  
QY 1021 TGGTACAGTACAGCTTTTGGCTACAGTGTCTCAATTCATTTTCAATTCCTTCTATATAC 1080  
DB 1081 TGGTACAGTACAGCTTTTGGCTACAGTGTCTCAATTCATTTTCAATTCCTTCTATATAC 1140  
QY 1081 CCTTTTGGCCACAGACGTTTCCAGAGGCTTTCTGGAAGATCTCTGTGTGACAAAGCAA 1140  
DB 1141 CCTTTTGGTCCAGAGCGTTTCCAGAGGCTTTCTGAGAGATCTTTGTGTGACAAAGCAA 1200  
QY 1141 CCAGCAGCTTTCACAGACCCAGTCAAGTATCTTCTTGA 1176  
DB 1201 CCAGCGCTGTCCAGAGAACAGTCAAGTATCTTCTTGA 1236  
RESULT 4  
AAI67750  
ID AAI67750 standard; cdna; 1173 BP.  
XX AC AAI67750;  
XX AC AAI67750;  
XX DT 27-FEB-2002 (first entry)  
XX XX Human histamine H4 receptor protein encoding cdna.  
DE DE Histamine receptor; H4; antirheumatic; antiarthritic; immunosuppressive;  
KW KW antiasthmatic; antiallergic; neuroprotective; antidiabetic; human;  
KW KW cerebroprotective; cAMP modulator; gene therapy; ss.  
XX OS Homo sapiens.  
XX Key Location/Qualifiers  
FT CDS 1..1173  
FT FT /\*cag= a  
FT FT /product= "histamine H4 receptor"  
XX WO200185786-A2.  
XX 15-NOV-2001.  
XX 04-MAY-2001; 2001WO-US014527.  
XX 05-MAY-2000; 2000US-0202151P.  
PR



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PR 12-NOV-1998; 98US-0108029P.
PR 20-NOV-1998; 98US-0109213P.
PR 27-NOV-1998; 98US-0110606P.
PR 16-FEB-1999; 99US-0120416P.
PR 26-FEB-1999; 99US-0121852P.
PR 12-MAR-1999; 99US-0123944P.
PR 12-MAR-1999; 99US-0123945P.
PR 12-MAR-1999; 99US-0123946P.
PR 12-MAR-1999; 99US-0123948P.
PR 12-MAR-1999; 99US-0123949P.
PR 12-MAR-1999; 99US-0123951P.
PR 28-MAY-1999; 99US-0136436P.
PR 28-MAY-1999; 99US-0136437P.
PR 28-MAY-1999; 99US-0136439P.
PR 28-MAY-1999; 99US-0137127P.
PR 28-MAY-1999; 99US-0137131P.
PR 28-MAY-1999; 99US-0137567P.
PR 28-JUN-1999; 99US-0141448P.
PR 27-AUG-1999; 99US-0151114P.
PR 03-SEP-1999; 99US-0152524P.
PR 28-SEP-1999; 99US-0156555P.
PR 28-SEP-1999; 99US-0156634P.
PR 28-SEP-1999; 99US-0156633P.
PR 28-SEP-1999; 99US-0156653P.
PR 01-OCT-1999; 99US-0157280P.
PR 01-OCT-1999; 99US-0157281P.
PR 01-OCT-1999; 99US-0157282P.
PR 01-OCT-1999; 99US-0157293P.
PR 01-OCT-1999; 99US-0157294P.
PR 12-OCT-1999; 99US-00416760.
PR 12-OCT-1999; 99US-00417044.
XX
XX
PA (AREN-) ARENA PHARM INC.
XX
XX
PI Bahan DP, Lehmann-Bruiensma K, Chalmers DF, Chen R, Dang HT;
PI Gore M, Liaw CW, Lin I, Lowitz K, White C;
XX
XX
DR WPI; 2000-317986/27.
DR P-PSDB; AAB02831.
XX
PT Non-endogenous, human G protein-coupled receptors for screening receptor,
PT inverse or partial agonists useful as therapeutic agents.
XX
XX
PS Example 1; Page 88-89; 187pp; English.
XX
CC The present invention describes transmembrane receptors, preferably human
CC G protein coupled receptors (GPCR), for which the endogenous ligand is
CC unknown (orphan GPCR receptors). More specifically the present invention
CC relates to non-endogenous, constitutively activated versions of a human
CC GPCR. These non-endogenous human GPCRs can be useful for the direct
CC identification of candidate compounds as receptors agonists, inverse
CC agonists or partial agonists for use as pharmaceutical agents. AAA46017
CC to AAA46126 and AAB02825 to AAB02859 represent sequences used in the
CC exemplification of the present invention
XX
SQ Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;
Query Match 56.9%; Score 669; DB 3; Length 1173;
Best Local Similarity 74.2%; Pred. No. 3.8e-206;
Matches 875; Conservative 0; Mismatches 295; Indels 9; Gaps 2;
QY 1 ATGTCGGAGTCTAACGGCAGCTGCTTGGCACTGCTCAAGTCCCTCGGCATTT 60
DB 1 ATGCCAGATCTATAGACAAATCAATTTATCATAGCACTCGTTTACTTTAGCATTT 60
QY 61 TTAATGTCCTGCTGCTTTGCTATACGATAGGCAATGCTGTGTCATTTAGCCCTTT 120
DB 61 TTTATGTCCTTAGTAGCTTTTGCTATAATGCTAGGAAATGCTTTGGTCATTTAGCTTT 120
QY 121 GTAGCAGACAGAAACCTTAGCATCGAAGTAATTTATTTTCTTAATTTGGCTATTCT 180
DB 121 GTGGTGACAAAAACCTTAGACATCGAAGTAGTATTATTTTCTTAACTTGGCCATCTCT 180
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RESULT 6

AAD01124

ID AAD01124 standard; cDNA; 1173 BP.

XX

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QY 181 GACTTCTTGGTGGTGTCTCATCTCCATTTCTCTGTAGATCCCTCACAGCGTGTAACTGG 240
DB 181 GACTTCTTGGTGGTGTGATCTCAATTCCTTTGTATCATCCTCACAGCGTGTGAAATGG 240
QY 241 AATTTTGGAAAGTGAATCTGCATGTTTGGCTCAATTACTACTGACTATCTTTTGTGCACAGCA 300
DB 241 GATTTTGGAAAGGAATCTGTGTATTTTGGCTCACTACTGACTATCTGTATATGACAGCA 300
QY 301 TCCGCTACAGTATTTGCTCTCATTAAGTACGATGATACAGTACAGTTCCTCAAGCGTGTG 360
DB 301 TCTGTATATAACATTTGCTCTCATCAGCTATGATCGATACCTGTGCTCAAAATGCTGTG 360
QY 361 CGTTATAGACACAGCAGCAGCTGGCATCTCGAATTTGCTCAAAATGCTGGTGTGTTGG 420
DB 361 TCTTATAGAACTCAACATACCTGGGGTCTTGAAGATTGTTACTCTGATGGTGGCGTGTGG 420
QY 421 ATACTGGCTTTCTTGGTCAATGGCCCAATGATTTCTGGCTTTGGATTTCTTGGAAAGACAGC 480
DB 421 GTGCTGGCTTTCTTAGTGATGGCCCAATGATTTCTAGTTTCAGAGTCTTGGNAGGA --- 476
QY 481 ACCAACACAGAGGAGTGCAGCGCTGGCTTTGTTACTGAGTGGTACATCTCTCGCCATTACA 540
DB 477 - - TGAAGGTAGTGAATGTGAACCTGGATTTTTCGGAATGGTACATCTTGCATCACA 534
QY 541 GCATTTCTTGAATTCCTGCTCCCTGCTCTCCCTGCTCTGCTGCTCTATTTCACTGTACAGATTAC 600
DB 535 TCATTTCTTGAATTTCTGATGATCCAGTCATCTTAGTCGCTTATTTCAACATGAATATTAT 594
QY 601 TGGAGCCTGTGGAAGCGTGGAGTCTCAGTAGGTGCTTACAGCAGTTCAGTTCAGTTCATCGCT 660
DB 595 TGGAGCCTGTGGAAGCGTGTATCATCTCAGTAGGTGCTTCAAGCCATCTCTGACGACTGCT 654
QY 661 ACCTTCTCAGGGGCACTGACACTCAGCAGAACTGGGTGGTGGTGTAGAGCAAGTCTTT 720
DB 655 GTCTCTTCCAAACATCTGTGGACACTCATTTCCAGAGGTAGACTATCTTCAAGGAGATCTCTT 714
QY 721 CCTGGATTAAAGGAACCCAGCGCATCCTTTCAATTCAGAAAGTCCACGAGGAAGAGCAGT 780
DB 715 TCTGCATCGACAGAGTTCCTGTCATCTTTTCAATTCAGAGAGACAGAGGAGAGAGTAGT 774
QY 781 CTCTGTGTCTTAAAGGACTCAGTAGCGGTAGTATCATCGCTTTCAAAGTGGGTTC 840
DB 775 CTCAATGTTTTCTCAAGAACCAAGATGAATAGCAATACAAATTTGCTTCAAAATGGGTTC 834
QY 841 TTCTGCGCATCAGAAAGCCAGTGTCTCAGCAGAGAGACAGTGGAGCTTCTCAGAGGC 900
DB 835 TTCTCCCAATCAGATTTCTGTAGCTCTTCAACAAAGGGAACATGTTGAACCTGCTTAGAGCC 894
QY 901 AGGAAGCTAGCAGGTGCTGCTGCTCTGAGTGTCTTTTGCAATTTGCTGGGCTCCG 960
DB 895 AGGAGATTAGCAGTCACTGGCCATTTCTTAGGGGTTTTTGTGTTTGTGGGCTCCA 954
QY 961 TATTGCTGTTCACAAATTTGTTCTTCAACTTATGCGAGAGGGGAGCCGCCCAATCGATT 1020
DB 955 TATTCTCTGTTCACAATTTGCTTTTCACTTTTATTTCTCAGCAACAGGTCCTTAAATCAGTT 1014
QY 1021 TGGTACAGCATAGCTTTTGGCTACAGTGTTCATTTCACTTATTAATCCCTTTCTATAC 1080
DB 1015 TGGTATAGAAATGCAATTTTGGCTTCACTGTTCAATTTCTTGTGCAATCTCTTTTGTAT 1074
QY 1081 CCTTTGTGCCACAGAGCTTTTCCAGAGCGCTTTCTGGAAGACTCTCTGTGTGACAAAGCAA 1140
DB 1075 CCATTGTGTCAAGCGCTTTCAAAGCGCTTTCTTGAANAATATTTTGTATATAAAGCAA 1134
QY 1141 CCAGCACCTTC - - ACAGACCCAGTCAATGATCTTCTTGA 1176
DB 1135 CCTCTACCATCAACAAACACAGTCGGTCAAGTATCTTCTTAA 1173
```

AC AAD01124;  
XX 02-NOV-2000 (first entry)  
XX Human orphan G protein-coupled receptor hrUP7 cDNA.  
XX  
XX Human; orphan G protein-coupled receptor; GPCR; hrUP7; drug screening;  
XX transmembrane receptor; signal cascade; ss.  
XX  
XX Homo sapiens.  
XX  
XX Key Location/Qualifiers  
XX CDS 1..1173  
XX /\*tag= a  
XX /product= "hrUP7"  
XX /note= "Human orphan G protein-coupled receptor"  
XX  
XX W0200031258-A2.  
XX  
XX 02-JUN-2000.  
XX  
XX 13-OCT-1999; 99WO-US023687.  
XX  
XX 20-NOV-1998; 98US-0109213P.  
XX 16-FEB-1999; 99US-0120416P.  
XX 26-FEB-1999; 99US-0121852P.  
XX 12-MAR-1999; 99US-0123946P.  
XX 12-MAR-1999; 99US-0123949P.  
XX 28-MAY-1999; 99US-0136436P.  
XX 28-MAY-1999; 99US-0136437P.  
XX 28-MAY-1999; 99US-0136439P.  
XX 28-MAY-1999; 99US-0136567P.  
XX 28-MAY-1999; 99US-0137127P.  
XX 28-MAY-1999; 99US-0137131P.  
XX 29-JUN-1999; 99US-0141448P.  
XX 29-SEP-1999; 99US-0156555P.  
XX 29-SEP-1999; 99US-0156633P.  
XX 29-SEP-1999; 99US-0156653P.  
XX 01-OCT-1999; 99US-0157280P.  
XX 01-OCT-1999; 99US-0157281P.  
XX 01-OCT-1999; 99US-0157282P.  
XX 01-OCT-1999; 99US-0157293P.  
XX 01-OCT-1999; 99US-0157294P.  
XX 12-OCT-1999; 99US-00416760.  
XX 12-OCT-1999; 99US-00417044.  
XX  
XX (AREN-) ARENA PHARM INC.  
XX  
XX Chen R, Dang HT, Liaw CW, Lin I;  
XX  
XX WPI; 2000-400068/34..  
XX P-PSDB; AAY71297.  
XX  
XX Novel human Orphan G protein-coupled receptors and the encoding cDNAs for  
XX use in the identification of G protein-coupled receptor agonists.  
XX  
XX Claim 25; Page 59; 102pp; English.  
XX  
XX The present sequence is a cDNA encoding hrUP7, an endogenous human orphan  
XX G protein-coupled receptor (GPCR). The full length hrUP7 cDNA was cloned  
XX by RT-PCR using human peripheral leucocyte cDNA as template. The orphan  
XX GPCR of the invention, like all GPCRs has seven transmembrane alpha  
XX helices with an extracellular N-terminus and an intracellular C-terminus.  
XX However, no endogenous ligands has yet been identified for the proteins  
XX of the invention. The orphan GPCR may be used in the identification of  
XX their endogenous ligands, and to screen potential GPCR agonists and  
XX antagonists for use as pharmaceutical agents. The proteins may also be  
XX used in the study of GPCR-mediated signalling cascades, and to elucidate  
XX their precise role in normal and diseased human conditions. Nucleic acid  
XX encoding human orphan GPCRs may be used for tissue localisation in  
XX expression analysis to provide information about their function in  
XX healthy and pathological states

XX SQ Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;  
XX  
XX Query Match 56.9%; Score 669; DB 3; Length 1173;  
XX Best Local Similarity 74.2%; Pred. No. 3.8e-206;  
XX Matches 875; Conservative 0; Mismatches 295; Indels 9; Gaps 2;  
XX  
XX QY 1 ATGTCGGAGTCTAAGCGACCTGAGCTCTTGCCACTGACTGCTCAAGTCCCTTGSCATTTT 60  
XX DB 1 ATGCCAGATACATAAGCACAATCAATTTATATCTAAGCACTCGTGTCTTTAGCATTTT 60  
XX  
XX QY 61 TTAATGTCCTGCTTGTCTTTGCTATAACGATAGCAATGCTGTGCTCAATTTAGCCCTTT 120  
XX DB 61 TTTATGTCCTTAGTAGCTTTTGTCTATAATGCTAGGAATGCTTTGGTCAATTTTAGCTTT 120  
XX  
XX QY 121 GTACGACAGAAACCTTAGACATCGAAGTAATATTTTCTTAATTTTAAATTTGGCTAATTTCT 180  
XX DB 121 GTGTGGACAAAACCTTAGACATCGAAGTAGTATTTTCTTAATTTTAACTTTGGCCATCTCT 180  
XX  
XX QY 181 GACTTCTTGTGGGTGTCATCTCCATTCCTCTGTACATCCCTCACACGCTGTTTAACTGG 240  
XX DB 181 GACTTCTTGTGGGTGTCATCTCCATTCCTTTGTACATCCCTCACACGCTGTTCGAATGG 240  
XX  
XX QY 241 AATTTGGAAGTGAATCTGCATGCTTTTGGCTCAATCTACTGACTATCTTTTGTGCACAGA 300  
XX DB 241 GATTTTGGAAAGGAAATCTGTGTATTTTGGGCTCACTACTGACTATCTCTTTATGACAGA 300  
XX  
XX QY 301 TCCGTCTACAGTATTTGCTCTCATTTAGCTACGATCGATACCACTGAGTTTCAAGCGCTGTG 360  
XX DB 301 TCTGTATATAACATTTGCTCTCATCAGCTATGATCGATACCTGTGACGCTCAATGCTGTG 360  
XX  
XX QY 361 CGTTATAGAGCACAGCACACTGGCATCTGAAATTTGTTGCTCAAAATGGTGGCTGTTTGG 420  
XX DB 361 TCTTATAGAACTCAACATACTCTGGGCTTTGAAGATTTGTTACTCTGATGCTGGCCGTTTGG 420  
XX  
XX QY 421 ATACTGGCTTTCTTGGTCAATGGCCCAATGATTTCTGGCTTGGATTCCTTGAAGAAGACAGC 480  
XX DB 421 GTGCTGGCTTTCTTAGTGAATGGCCCAATGATTTCTAGTTTTCAGAGTCTTGAAGAAG 476  
XX  
XX QY 481 ACCAACACAGAGGAGTGGAGCTGGCTTCTGTTACTGAGTGGTACATCTCGCCCATACA 540  
XX DB 477 --TGAAGGTAGTGAATGTAACCTGGATTTTTCGGNATGGTACATCTTGGCCATACA 534  
XX  
XX QY 541 GCATTCTTGGAAATTCCTGCTCCCTGCTCTCTTGGTGGTCTATTTTCAAGTGTACAGATTTAC 600  
XX DB 535 TCATTCTTGGAAATTCGTGATCCCATGTCATCTTAGTGGCTTATTTTCAACATGAATATTTAT 594  
XX  
XX QY 601 TGGAGCTGTGGAAAGCTGGGAGTCTGATAGTGGCTCTAGTGGCTCTAGCCGCTGGATTCATCGCT 660  
XX DB 595 TGGAGCTGTGGAAAGCTGGATCATCTCAGTAGGTGCCAAAGCCATCTCTGGACTGACTGCT 654  
XX  
XX QY 661 ACCTCTTCCAGGGGCACCTGGACACTCAGCAGAACTGGGTTGGCTTGTAGGACAGTCTT 720  
XX DB 655 GTCTCTTCCAAACATCTGTGGACACTCATTCAGAGGTAGACTATCTTCAAGAGATCTCTT 714  
XX  
XX QY 721 CCTGGATTAAGGAAACAGCCGATCCCTTCAATTCAGAAAGTCCACGAGGAAAGAGCAGT 780  
XX DB 715 TCTGCATCGACAGAAAGTTCTGTCATCTTTTCAATTCAGAGACAGAGAGAGAGAGTAGT 774  
XX  
XX QY 781 CTCCTGTGTCTTTAAGGACTCAATGAGCGGTAGTATCATCGCTTCAAAGTGGGTTC 840  
XX DB 775 CTCATGTTTTCTCAAGAACCAAGATGAATAGCAATACAATTTGCTTCCAAATAGGTTTC 834  
XX  
XX QY 841 TTTCTCCGATCAGAAAGCCCATGCTTCCACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900  
XX DB 835 TTTCTCCCAATCAGATTTCTGTAGCTCTTCCAAAGGGAACATGTTGAACATGCTTAGAGCC 894  
XX  
XX QY 901 AGGAAGCTAGCCAGGTGCTAGCTGCTCTCTCTGAGTGTCTTTTGGCATTTGCTGGGCTCCG 960  
XX DB 895 AGGAGATTAGCAAGTCACTGCTGCTCTCTTAGGGGTTTTTGTGTTTGTGCTGGGCTCCA 954  
XX  
XX QY 961 TATTGCTGTTCACAAATGTTGTTTCAACTTATCGCAGAGGGGAGCGCCCAATTCGATT 1020  
XX

Db 955 TATTCTCTGTTCAAAATGTCCTTTCTTATTTTATTCCTCAGCAACAGGCTCTAAATCAGTT 1014  
 Qy 1021 TGGTACAGCATAGCTTTTGGCTACAGTGGTTCAGTTCAATTCACCTTATTAATCCCTTTCTATAC 1080  
 Db 1015 TGGTATAGAAATGCATTTTGGCTTCAGTGGTTCAAATTCCTTTGTCAATCCTCTTTTGTAT 1074  
 Qy 1081 CTTTGTGCCACAGACGTTTCCAGAGGCTTTTCGGAAGATACCTGTGTGACAAAGCAA 1140  
 Db 1075 CCATTGTGTCAAGCGCTTTCAAAGGCTTTCTTGAAATATTTTGTATATAAAGCAA 1134  
 Qy 1141 CCAGCACCTTC---ACAGACCCAGTCAAGTATCTTCTTGA 1176  
 Db 1135 CCTCTACCATCAACACAGCTGGTCAAGTATCTTCTTAA 1173

## RESULT 7

AAF83203  
 ID AAF83203 standard; CDNA; 1173 BP.

AC AAF83203;

DT 09-JUL-2001 (first entry)

XX Human GPCR-like polypeptide, PFI-013 encoding cDNA.

XX G-protein coupled receptor; GPCR; PFI-013; antiallergic; antispasmodic;  
 KW antiinflammatory; vasotropic; antidiabetic; anorectic; cytostatic; human;  
 KW osteopathic; neuroprotective; nootropic; dermatological; gynecological;  
 KW signal transduction; ss.

XX Homo sapiens.

XX Key Location/Qualifiers  
 FT CDS 1..1173  
 FT /\*tag= a  
 FT /product= "PFI-013"

XX BP1096009-A1.

XX 02-MAY-2001.

XX 24-OCT-2000; 2000EP-00309364.

XX 29-OCT-1999; 99GB-00025641.

XX 20-APR-2000; 2000GB-00009973.

XX (PFI2 ) PFIZER LTD.

XX (PFI2 ) PFIZER INC.

XX Peter B, O'reilly MA;

XX WPI; 2001-309854/33.

XX P-PSDB; AAB62445.

XX New G-protein coupled receptor-like polypeptide, polynucleotide for  
 PT screening drug candidates for treating diseases associated with signal  
 PT transduction e.g. allergic, inflammatory, pulmonary, pulmonary, neoplastic diseases.

PS Claim 1; Page 43; 66pp; English.

XX This cDNA of NCIMB 41073 encodes a human G-protein coupled receptor  
 CC (GPCR)-like polypeptide, designated PFI-013. The PFI-013 protein can be  
 CC expressed by standard recombinant methodology. Antibodies and modulators  
 CC of PFI-013 are useful in the manufacture of a medicament for treating  
 CC allergic disorder, including extrinsic asthma, immunological disorders,  
 CC such as intrinsic asthma, vasculitic granulomatous disease, interstitial  
 CC and other pulmonary disease, including chronic obstructive pulmonary  
 CC disease (COPD), infectious, inflammatory disease, such as inflammatory  
 CC bowel disease and neoplastic and myeloproliferative diseases. They are  
 CC also useful for treating obesity, diabetes, metabolic, neurological  
 CC diseases, psychotherapeutics, urogenital disease, reproduction and sexual  
 CC medicine, inflammation, cancer, tissue repair, dermatology, photoaging,  
 CC skin pigmentation, osteoporosis, cardiovascular, gastrointestinal

CC diseases, allergy and respiratory disease, sensory organ disorders, sleep  
 CC disorders and hair loss. The PFI-013 protein and nucleic acid are useful  
 CC in the diagnosis and treatment of the above conditions and also for  
 CC screening drug candidates for the treatment of diseases associated with  
 CC signal transduction. The antibodies are also useful for enrichment of  
 CC eosinophils from mammalian, especially human blood and for detecting the  
 CC protein in biological samples

XX Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;

Query Match 56.9%; Score 669; DB 4; Length 1173;  
 Best Local Similarity 74.2%; Pred. No. 3.8e-206;  
 Matches 875; Conservative 0; Mismatches 295; Indels 9; Gaps 2;

Qy 1 ATGTCGGAGTCTAACGGCACTGAGCTCTTGCCACTGACTGCTCAAGTCCCTTGGCAATTT 60  
 Db 1 ATGCCAGATACATAATAGCAACAATCAATTTATCACTAAGCACTCGTGTACTTTAGCAATTT 60  
 Qy 61 TTAATGTCCTGCTTGTCTTTTGTCTATAACGATAGGCAATGCTGTGGTCATTTTAGCCTTT 120  
 Db 61 TTTATGTCCTTAGTAGCTTTTGTCTATAATGCTAGGAAATGCTTTGGTCATTTTAGCCTTT 120  
 Qy 121 GTACAGACAGAAACCTTAGACATCGAAGTAATATTTTCTTAATTTGGCTATTCT 180  
 Db 121 GTGTGGACAAAACCTTAGACATCGAAGTAGTTATTTTCTTAATTTGGCCATCTCT 180  
 Qy 181 GACTTCTTCGTGGGTGTCATCTCCATTCCTCTGTACATCCCTCACACGCTGTTTAACTGG 240  
 Db 181 GACTTCTTCGTGGGTGTCATCTCCATTCCTCTGTACATCCCTCACACGCTGTTTAACTGG 240  
 Qy 241 AATTTTGGAAAGTGGAAATCTGCATGTTTGTGCTCAATTAATGACTATCTTTTGTGCACAGCA 300  
 Db 241 GATTTTGGAAAGAAATCTGTGTTATTTTGTGCTCAATTAATGACTATCTTTTGTGCACAGCA 300  
 Qy 301 TCCGTCTACAGTATTGTCCTCATTAGCTACGATCGATACCAGTCAGTTTCAAACGCTGTG 360  
 Db 301 TCTGTATATAACATTTGCTCTCATCAGCTATGATCGATACCTGTGTCAGTCTCAAATGCTGTG 360  
 Qy 361 CGTTATAGACACAGCACACTGGCATCTGAAAATTTGTTGCTCAAAATGGTGGCTTTGG 420  
 Db 361 TCTTATAGAACTCAACATACCTGGGGTCTTGAAGATTGTTACTCTGTAGTGGTGGCGTTGG 420  
 Qy 421 ATACTGGCTTTCTTGGTCAATGGCCCAATGATCTGGCTTCGGATTCTTGGAAACACAGC 480  
 Db 421 GTGCTGGCCTTCTTAGTGAATGGCCCAATGATCTAGTTTTCAGAGTCTTGAAGA 476  
 Qy 481 ACCAACACAGAGGAGTCGGAGCCTGGCTTTGTTACTAGTGGTGAATCATCTCGCCATTACA 540  
 Db 477 --TGAAGGTAGTGAATGTGAACCTGGATTTTTCGGAAATGGTACATCTTGCATCACA 534  
 Qy 541 GCATTTCTGGAAATTCCTGCTCCCTGCTCTCTGTTGGTGTCTATTTCAGTGTACAGATTAC 600  
 Db 535 TCATTTCTGGAAATTCGTGATCCAGTCACTCTTGTAGTGGTGTATTTTCAACATGAATTTAT 594  
 Qy 601 TGGAGCCTGTGGAAAGCCTGGAGTCTCAGTAGGTGCTCCTAGCCCTAGCCACGCTGGATTTCGCT 660  
 Db 595 TGGAGCCTGTGGAAAGCCTGATCATCTCAGTAGGTGCCAAGCCATCTCTGGACTGCTGCT 654  
 Qy 661 ACCTTTCCAGGGGCACTGGACACTCACGGAGAACTGGTGTGGTGTGTAGGACAAAGTCTT 720  
 Db 655 GTCTTCTTCAACATCTGTGGACACTCAATTCAGAGGTAGACTATCTTCAAGGAGATCTCTT 714  
 Qy 721 CCTGGATTAAAGGAACAGCCGATCCCTTCATTCAGAAAGTCCACAGGAAAGAGCAGT 780  
 Db 715 TCTGCACTCGACAGAAAGTTCCTGCACTCTTCAATTCAGAGAGACAGAGAGAAAGAGTAGT 774  
 Qy 781 CTCCTGTGTCTTAAAGACTCACATAGGGGTAGTATCATCGCTTCTCAAAGTGGTTC 840  
 Db 775 CTCAATGTTTCTCAAGAACCAAGATCAATAGCAATCAATTTGCTTCAAAATGGTTC 834  
 Qy 841 TTCTGCCGATCAGAAAGCCCGCTCTCACAGAGAGACAGCTGGAGCTCTCTCAGAGGC 900  
 Db 835 TTCTCCCAATCAGATTCTGTAGCTCTTTCACCAAGGGGAACATGTTGAACCTGCTTAGAGCC 894





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Db 361 TCCTATAGAACTCAACATCTGGGCTCTGAAGATTGTTACTCTGATGGTGGCGTTGG 420
Qy 421 ATACTGGCTTTCTTGGTCAATAGGCCCAATGATCTCGCTCGGATTCCTGGAAAGAACAGC 480
Db 421 GTGCTGGCTTTCTTAGTGAATGGCCCAATGATCTAGTTTCTAGAGTCTTGGAAAGAA 476
Qy 481 ACCAACACAGAGGAGTGGAGCGCTGGCTTTGTTACTGAGTGGTACATCCTCGCCATTACA 540
Db 477 -TGAAGGTAGTGAATGTGAACCTGGATTTTTTCGGAAATGGTACATCCTTGGCATCACA 534
Qy 541 GCATTTCTTGAATTCCTGCTCCCTGCTCTCTCTGCTGCTCTATTTTCAGTGACAGATTATAC 600
Db 535 TCATTTCTTGAATTCGTGATCCCAAGTCATCTTAGTGGCTTATTTCAACATGAATATTAT 594
Qy 601 TGGAGCTGTGGAGCGTGGAGTCTCAGTAGTGGCTTACCCAGCCAGCGTGAATCATCGCT 660
Db 595 TGGAGCTGTGGAGCGTGGATCATCTCAGTAGTGGCTCAAGAGCCATCTGGAGTACTGCT 654
Qy 661 ACCTTTCCAGGGCACTGGACACTCAGCAGACTCGGTGGCTTGTAGGACAGTCTT 720
Db 655 GTCTCTTCCAACTCTGTGACACTCATTCAGAGGTAGACTATCTTCAAGGAGATCTCTT 714
Qy 721 CCTGGATTAAAGGAACAGCGGCTCTCTTCAATCAGAAAGTCCACGAGGAAGAGCAGT 780
Db 715 TCTGATCGACAGAGTTCCTGCACTCTTTCATTCAGAGACAGAGAGAGAGTAGT 774
Qy 781 CTCTGTGTCTTAAAGACTCAATGAGCGGTAGTATCATCGCTTCAAAAGTGGGTCC 840
Db 775 CTATGTTTTCTCAAGAACCAAGATGAATAGCAATACAATTTGCTTCCAAATGGGTCC 834
Qy 841 TTCTGCCATCAGAAAGCCAGTCTTCCAGAGAGACAGCTGGAGCTTCTCAGAGGC 900
Db 835 TTCTCCCAATCAGATTCTGTAGCTCTTCAAGAGGAAATGTTGAAGTCTTAGAGCC 894
Qy 901 AGGAAGCTAGCCAGTCTGCTGCTCTGAGTGTCTTTGCTGCTTTGCTGGCTCCG 960
Db 895 AGGATATTAGCAAGTCACTGGCCATTTCTTAGGGGTTTTGCTGTTGCTGGCTCCA 954
Qy 961 TATGCTGTTCACAAATGTTTTCAACTTATCGCAGAGGGGAGCGCCCAATCGATT 1020
Db 955 TATCTCTGTTCACAAATGCTTTTCAATTTATTCCTCAGCAACAGGTCTCTAAATCAGTT 1014
Qy 1021 TGGTACAGCATAGCTTTTGGCTACAGTGGTTCATTCATTTATTAATCCTTCTATAC 1080
Db 1015 TGGTATAGAAATGCAATTTTGGCTTCAAGTGGTTCATTTCTTGTCAATCTCTTTGTAT 1074
Qy 1081 CCTTTGTGCCACAGACGTTTCCAGAGGCTTTCTGGAAGATACCTGTGTGACAAAGCAA 1140
Db 1075 CCATTGTGTCAAGCGCTTTCAAGAGGCTTTCTTGAATAATTTTGTATAAAGAAACAA 1134
Qy 1141 CCAGCACCTTC---ACAGACCGATCAGTATCTTCTTGA 1176
Db 1135 CCTTACCATCACAAACAGTCGCTCAGTATCTTCTTAA 1173
```

## RESULT 9

AB280663

ID AB280663 standard; cdna; 1173 BP.

XX AC

AC AB280663;

XX DT

13-JUN-2003 (first entry)

XX DE

Human histamine receptor coding sequence.

XX KW

human; histamine receptor; gene; ds; chromosome 18; anti-inflammatory;  
anti-asthmatic; anti-allergic; dermatological; cerebroprotective; stroke;  
anti-migraine; cardiant; anti-rheumatic; anti-arthritis; antipsoriatic;  
neuroprotective; inflammation; asthma; allergy; atopic dermatitis;  
myocardial infarction; migraine; chronic obstructive pulmonary disease;  
rheumatoid arthritis; multiple sclerosis; inflammatory bowel disease;  
psoriasis; receptor.







```
Db 301 TCTGTATATACATTTGCTCTCATGAGCTATGATCGATACCTGTGTCAGTCTCAATGCTGTG 360
Qy 361 CGTTATAGACACAGCACACCTGGCATCTGAAATTTGTTGCTCAAAATGCTGCTGTTTGG 420
Db 361 TCTTATAGAACTCAACATCTGGGCTCTGAAGATTTGTTACTCTGATGGTGGCCGTTTGG 420
Qy 421 ATACTGGCTTTCTTGGTCAATGGCCCATGATCTTGGCTTCGGATTTCTTGGAGAACACAGC 480
Db 421 GTGCTGGCTCTTCTTAGTGAATGGGCAATGATTTCTAGTTTCAGAGTCTTGGAAAGGA---- 476
Qy 481 ACCAACACAGAGGAGTGGAGCTGGCTTGTGTTACTGAGTGGTATCATCTCGCCATTACA 540
Db 477 --TGAAGTAGTGAATGGTGAATTTTTCGGAAATGGTATCATCTTGGCATCACA 534
Qy 541 GCATTTCTTGAATTCCTGCTCCCTGCTCTTCTTGGTGGTCTATTTCAAGTGTACAGTTTAC 600
Db 535 TCATTTCTTGAATTCGTCATCCCATCATCTTCTAGTGGCTTATTTCAACATGAATTTAT 594
Qy 601 TGGAGCCTGTGGAAGCGTGGAGTCTCAGTAGTGGCTTGGCTTGGTGTAGCACAGTCTT 660
Db 595 TGGAGCCTGTGGAAGCGTGGATCTCAGTAGTGGCTTGGCTTGGTGTAGCACAGTCTT 654
Qy 661 ACCTCTTCCAGGGGCACTGGACACTCAGCGAGAACTGGGTTGGCTTGGTGTAGCACAGTCTT 720
Db 655 GTCTCTTCCACATCTGTGGACATCTATTAGAGTAGACTATCTTCAAGGAGATCTCTT 714
Qy 721 CCTGGATTAAGGAACCGCCGCTCTTCTTCAATCAGAAATGCCAGGAGAAAGAGT 780
Db 715 TCTGCATCGACAGAAATTCCTGCTCTTCTTCAATCAGAGACAGAGGAGAAAGTAGT 774
Qy 781 CTCTGTGCTCTTAAGGACTCACATGAGCGGTAGTATCATCGCTTCAAAAGTGGTTCC 840
Db 775 CTCTATGTTTCTCAAGAACCAAGATGAATAGCAATACAATTTGCTTCCAAATGGGTTCC 834
Qy 841 TTCTGCCGATCAGAAAGCCAGTCTTCCACAGAGAGACACETGGAGCTTCTCAGAGGC 900
Db 835 TTCTCCCATCAGATCTGTAGTCTTCCACCAAGGAAACATGTTGAATGCTTTAGAGCC 894
Qy 901 AGGAAGCTAGCCAGTCTGCTAGCTGTCTCTGAGTGTCTTTGGCAATTTGCTGGGCTCG 960
Db 895 AGGAGATTAGCAAGTCACTGGCCATCTCTTAGGGGTTTTTGTGTTGCTGGGCTCA 954
Qy 961 TATTGCTGTTCAATTTGTTCTTCACTTATCGCAGAGGGAGGCCCCCAATTCGATT 1020
Db 955 TATTCTGTTTCAATTTGTTCTTCACTTATTTTCTCAGCAACAGGTCCTTAAATCAGTT 1014
Qy 1021 TGGTACAGTAGCTTTTGGCTACAGTGTCTCAATTCACCTTATTAATCCCTTTCTATAC 1080
Db 1015 TGGTATAGATGATTTTGGCTTCAAGTGTCTCAATTCCTTGTCAATCTCTTTTGTAT 1074
Qy 1081 CCTTTGTGCCACAGACGTTTCCAGAGGCTTTCTGGAAGATACCTGTGTGACAAAGCAA 1140
Db 1075 CCATTGTGTCAAGCGCTTTCAAAGGCTTTCTGGAATATTTGTATATAAAGCAA 1134
Qy 1141 CCAGACCTTC---ACAGACCCAGTCAATCTCTTTGA 1176
Db 1135 CCTTACCATCAACACAGTCGCTCAGTATCTCTTAA 1173
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## RESULT 12

ACA93262

ID ACA93262 standard; cDNA; 1173 BP.

XX

AC ACA93262;

XX

DT 16-JUL-2003 (first entry)

XX

DE Human cDNA encoding GPCR hrUP7.

XX

Human; ss; gene; orphan G protein-coupled receptor; GPCR; hARE-3; hARE-4;  
hARE-5; hrUP3; hrUP5; hrUP6; hrUP7; hGPCR27; hARE-1; hARE-2; hrPRL; hG2A;  
hCHN3; hCHN4; hCHN6; hCHN8; hCHN9; hCHN10; hrUP4; signalling cascade.

XX

OS Homo sapiens.  
XX US2003017528-A1.  
XX 23-JAN-2003.  
XX  
XX 06-JUN-2001; 2001US-00875076.  
XX  
PR 20-NOV-1998; 98US-0109213P.  
PR 16-FEB-1999; 99US-0120416P.  
PR 26-FEB-1999; 99US-0121852P.  
PR 12-MAR-1999; 99US-0123946P.  
PR 12-MAR-1999; 99US-0123949P.  
PR 28-MAY-1999; 99US-0136436P.  
PR 28-MAY-1999; 99US-0136437P.  
PR 28-MAY-1999; 99US-0136567P.  
PR 28-MAY-1999; 99US-0137127P.  
PR 28-MAY-1999; 99US-0137131P.  
PR 29-JUN-1999; 99US-014448P.  
PR 28-SEP-1999; 99US-0156333P.  
PR 29-SEP-1999; 99US-0156555P.  
PR 29-SEP-1999; 99US-0156634P.  
PR 12-OCT-1999; 99US-00417044.  
XX

(CHEN/) CHEN R.  
(DANG/) DANG H T.  
(LIAN/) LIAN C W.  
(LINI/) LIN I.

Chen R, Dang HT, Liaw CW, Lin I;

WPI; 2003-428952/40.

P-PSDB; ABU92265.

Novel endogenous, orphan, human G protein-coupled receptors useful for identification of modulators of the receptor and as research tools for understanding the role of the receptor in human body.

Claim 25; Page 22; 54pp; English.

The invention relates to a human G protein-coupled receptor (GPCR) appearing as ABU92259-ABU92277 (encoded by cDNAs ACA93256-ACA93274) named hARE-3, hARE-4, hARE-5, hrUP3, hrUP5, hrUP6, hrUP7, hGPCR27, hARE-1, hARE-2, hrPRL, hG2A, hCHN3, hCHN4, hCHN6, hCHN8, hCHN9, hCHN10 and hrUP4. Also included are a plasmid comprising a vector and one of the cDNAs above and a host cell comprising the plasmid. The GPCRs are useful for the direct identification of candidate compounds as inverse agonists, agonists or partial agonists. In vitro and in vivo systems incorporating GPCRs is useful for elucidating and understanding the roles these receptors play in the human condition, both normal and diseased, as well as understanding the role of constitutive activation as it applies to understanding the signalling cascade. The cDNAs are useful for making a probe for dot-blot analysis against tissue mRNA and/or RT-PCR identification of the expression of the receptor in tissue samples. The present sequence is a cDNA encoding a GPCR of the invention

SQ Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;

Query Match 56.9%; Score 669; DB 8; Length 1173;

Best Local Similarity 74.2%; Pred. No. 3.8e-206;

Matches 875; Conservative 0; Mismatches 295; Indels 9; Gaps 2;

Qy 1 ATGTCGGAGTCTAAGCGCAGTGTCTTGGCACTGCTCAAGTCCCTTGGCAATTT 60

Db 1 ATGCCAGATCTAATAGCAATCAATTTATCATTAGCACTGTGTACTTTAGCAAT 60

Qy 61 TTAATGTCCTGCTGCTTTTGTCTATAACGATAGCAATGCTGTGGTCAATTTAGCCTTT 120

Db 61 TTTATGCTCTTAGTAGCTTTTGTCTATAATGCTAGGAAATGCTTTGGTCAATTTAGCTTT 120

Qy 121 GTACACAGACAAACCTTAGCATCGAAGTAAATTTTCTTAATTTGGCTATTCT 180

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Db 121 GTGGTGGACAAAACCTTAGACATCGAAGTAGTATTTTCTTAACTTGGCCATCTCT 180
Qy 181 GACTTCTTGGTGGTGTCTCTCCATTCCTCTGTACATCCCTACACGCTGTTTAACTGG 240
Db 181 GACTTCTTGGTGGTGTCTCTCCATTCCTCTGTACATCCCTACACGCTGTTTAACTGG 240
Qy 241 AATTTTGGAAAGTGAATCTGCATGTTTTGGCTCAATTAAGTCTGACTACTCTTTTGTGCACAGCA 300
Db 241 GATTTTGGAAAGGAAATCTGTGATTTTGGCTCAATTAAGTCTGACTACTCTTTTGTGCACAGCA 300
Qy 301 TCCGTCTACAGTATGTCCTCATTPAGCTACGATACGATACGATACGATTTCAAAAGCTGTG 360
Db 301 TCTGTATATAACATTTGTCCTCATCAGCTATGATCGATACGATACGATTTCAAAAGCTGTG 360
Qy 361 CGTTATAGACAGCAGCAGCAGCTGGCATCTGGAATTTGTTGCTCAAAATGTTGGTGGCTTTGG 420
Db 361 TCTTATAGAACTCAACATCTGGGGTCTTGAAGATTTGTTACTCTGATGGTGGCGGTTGG 420
Qy 421 ATACTGGCTTCTTGGTCAATGGCCCAATGATTCGTGCTTGGATTCCTTGGAAACAGC 480
Db 421 GTGCTGGCTTCTTAGTGAAATGGCCCAATGATTCGTGCTTGGATTCCTTGGAAAGCA 476
Qy 481 ACCAACACAGAGGAGTCGAGCTGGCTTTGTTACTGAGTGGTACATCCTCGCCATTACA 540
Db 477 -TGAAGGTAGTGAATGTGAACCTGGATTTTTCGGAATGGTACATCCTTGGCCATCACA 534
Qy 541 GCATTTCTGGAATTCCTGCTCCCTGTCTCCTTGGTGTCTATTTTCAGTGTACAGATTTAC 600
Db 535 TCATTTCTGGAATTCGTGATCCCAAGTCTCATCTAGTCTGCTTATTTTCAACATGAATTTAT 594
Qy 601 TGGAGCTGTGGAAGCTGGAGTCTCAGTAGGTGCTTACAGTGGTCCCTAGCCAGCTGGATTCATCGCT 660
Db 595 TGGAGCTGTGGAAGCTGTATCTCAGTAGGTGCTTACAGTGGTCCCAAGCCATCTTGGACTGCT 654
Qy 661 ACCTTTCCAGGGGCACTGGACATCTACGAGAACTGGTGGTGGTGTAGGACAAAGTCTT 720
Db 655 GTCTCTTCCAACATCTGTGACATCTATCAGAGGTAGACTATCTTCAAGGAGATCTCTT 714
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Db 715 TCTGCAATCGACAGAGTTCCTGCACTCTTCAATTCAGAGAGACAGAGAGAGAGTAGT 774
Qy 781 CTCTGCTGTCTTAAAGCACTCAGTGGCTGTATCTAGCTCTTCAAAAGTGGTTC 840
Db 775 CTGATGTTTCTCAAGAACCAAGATGAATAGCAATGATGCTTCAAAATGGGTTC 834
Qy 841 TTCTGCCGATCAGAAAGCCAGTGTCTTCAAGAGAGACAGTGGAGCTTCTCAGAGGC 900
Db 835 TTCTCCCAATCAGATTCGTAGCTCTTCAAAAGGGAACATGTTGAAGCTCTTAGAGCC 894
Qy 901 AGGAGCTAGCCAGGTGCTAGCTGTCTCTGAGTGTCTTTGCAATTTGCTGGGCTCCG 960
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Qy 1021 TGGTACAGCATAGCTTTTGGCTACAGTGGTCAATTCATTTAATTCCTTTCTATAC 1080
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Qy 1081 CCTTTGGCCACAGAGCTTTCCAGAGGCTTCTGGAAGATACCTGTGTGACAAAGCAA 1140
Db 1075 CCATTTGTCTCAAGAGCGCTTTCAAAAGGCTTCTTGAATAATTTTGTATAAAAAGCAA 1134
Qy 1141 CCAGCACTTC---ACAGACCCAGTCAATCTCTTTGA 1176
Db 1135 CCTTACCATCACACACAGTGGTCAATCTTCTTAA 1173
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RESULT 13  
ADG98759

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ID ADG98759 standard; cDNA; 1173 BP.
XX ADG98759;
AC ADG98759;
XX 11-MAR-2004 (first entry)
DT Human orphan GPCR cDNA, RUP7.
XX Human; G protein-coupled receptor; GPCR; research tool; gene; ss.
XX Homo sapiens.
OS
XX Key Location/Qualifiers
XX CDS 1..1173
FT /*tag= a
FT /product= "Human GPCR protein"
XX US2003148450-A1.
XX 07-AUG-2003.
XX 17-OCT-2002; 2002US-00272983.
XX 20-NOV-1998; 98US-0109213P.
XX 16-FEB-1999; 99US-0120416P.
XX 26-FEB-1999; 99US-0121852P.
XX 12-MAR-1999; 99US-0123946P.
XX 28-MAY-1999; 99US-0123949P.
XX 28-MAY-1999; 99US-0136436P.
XX 28-MAY-1999; 99US-0136437P.
XX 28-MAY-1999; 99US-0136439P.
XX 28-MAY-1999; 99US-0136567P.
XX 28-MAY-1999; 99US-0137127P.
XX 28-MAY-1999; 99US-0137131P.
XX 29-JUN-1999; 99US-0141448P.
XX 28-SEP-1999; 99US-0156333P.
XX 29-SEP-1999; 99US-0156555P.
XX 29-SEP-1999; 99US-0156634P.
XX 12-OCT-1999; 99US-00417044.
XX (CHEN/) CHEN R.
PA (DANG/) DANG H T.
PA (LIAW/) LIAW C W.
PA (LINI/) LIN I.
PI Chen R, Dang HT, Liaw CW, Lin I;
XX WPI; 2003-897571/82.
XX P-PSDB; ADG98760.
XX New cDNA encoding a human G protein coupled receptor, useful for making a
XX probe for dot-blot analysis against tissue-mRNA, and/or for RT-PCR
XX identification of the expression of the receptor in tissue samples.
XX Claim 25; SEQ ID NO 13; 52pp; English.
XX The present invention provides novel human G protein-coupled receptor
XX (GPCR) proteins and their encoding nucleic acids. The invention is useful
XX for making a probe for dot-blot analysis and for RT-PCR identification of
XX the expression of the receptor in tissue samples. The invention is also
XX useful for identifying candidate compounds as inverse agonists, agonists
XX or partial agonists and as research tools in determining the location of
XX the receptors within the body. The present sequence is human orphan G
XX protein-coupled receptor cDNA.
XX Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;
XX
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Query Match 56.9%; Score 669; DB 10; Length 1173;
Best Local Similarity 74.2%; Pred. No. 3.8e-206;
Matches 875; Conservative 0; Mismatches 295; Indels 9; Gaps 2;
Qy 1 ATGTCCGAGTCTAACGGCAGTCTTGGCACTGACTGCTCAAGTCCCTTGGCAATTT 60
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

Db 1 ATGCCAGATACATAAGACAAATCAATTTATCATAGCACTCGTGTCTTTTACATTTT 60  
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Db 61 TTTATGTCCTTTAGTAGCTTTTGCTATATATGCTAGGAATGCTTTGGTCAATTTTACGCTTTT 120  
Qy 121 GTACGAGACAAACCTTAGACATCGAAGTAATTTATTTTCTTAATTTGGCTATTTCT 180  
Db 121 GTGTGGACAAAACCTTAGACATCGAAGTAGTTATTTTCTTAATTTGGCTATTTCT 180  
Qy 181 GACTTCTTCGTGGGTGCTCATCTCTGTATACATCCCTCACAGCGCTGTTTAACTGG 240  
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Qy 481 ACCAACACAGAGGAGTGGAGCGCTGCTTGTACTGAGTGGTACATCTCGCCCATTAACA 540  
Db 477 --TGAAGGTAGTGAATGTGAACCTGGATTTTTCGGAATGGTACATCTTGGCCATACA 534  
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Db 535 TCATTTCTTGAATTCGTTGATCCAGTCACTTTAGTGGCTTTATTTCAACATGAATTTAT 594  
Qy 601 TGGAGCTGTGGAAGCGTGGGAGTCTCAGTAGGTGCTTCCCTAGCCAGCTGGATTCATCGCT 660  
Db 595 TGGAGCTGTGGAAGCGTGATCACTCAGTAGGTGCTTCCCAAGCCATCTTGGAGTCTGCT 654  
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Db 775 CTCATGTTTCTCAAGAACCAAGATGAATAGCAATACAAATTTGCTTCCAAATGGTTCC 834  
Qy 841 TTCTGCCGATCAGAAAGCCAGTGTTCACAGAGAGACAGTGGAGCTTCTCAGAGGC 900  
Db 835 TTCTCCCAATCAGATTTCTGTAGCTTTCACCAAGGGAACATGTGTGAAGTCTGTAGAGCC 894  
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## RESULT 14

ABS57063

ID ABS57063 standard; cDNA; 1173 BP.

XX ABS57063;

XX 28-JAN-2003 (first entry)

XX Human cDNA encoding G-protein coupled receptor AXOR35.

Human; ss; gene: G-protein coupled receptor; AXOR35; lymphocyte;  
macrophage; eosinophil; neutrophil; infection; transplant rejection;  
gastrointestinal disorder; gastric ulcer; inflammatory bowel disease;  
Crohn's disease; irritable bowel syndrome; vomiting; inflammation;  
atopic dermatitis; allergy; autoimmune disorder; rheumatoid arthritis;  
psoriasis; urological disease; urinary retention; cardiovascular disease;  
myocardial infarction; hypotension; hypertension; pulmonary disorder;  
chronic obstructive pulmonary disease; cough; renal disease;  
renal ischaemia; arteriosclerosis; atherosclerosis; psychosis;  
neurological disorder; migraine; anorexia; anxiety; schizophrenia;  
dyskinesia; Parkinson's disease; cancer; obesity; stroke; septic shock;  
graft versus host disease; osteoporosis.

XX Homo sapiens.

Key Location/Qualifiers  
CDS 1..1173

FT /\*tag= a

FT /product= "AXOR35"

FN US2002137054-A1.

XX 26-SEP-2002.

XX 20-JUL-2001; 2001US-00910411.

XX 02-NOV-1999; 99US-00431898.

XX 03-FEB-2000; 2000US-00497790.

XX 20-OCT-2000; 2000US-00693761.

XX (SMIK ) SMITHKLINE BEECHAM CORP.

XX (SMIK ) SMITHKLINE BEECHAM PLC.

XX Aubart KM, Bergsma DJ, Fitzgerald L, Graybill TL, Li X;

XX Michalovich D, Morrow DM, Zhu Y;

XX WPI; 2003-074982/07.

XX P-PSDB; ABG71960.

XX Novel isolated G-protein coupled receptor polypeptide, AXOR35, useful for

XX treating infections, gastrointestinal disorders, autoimmune disorders,

XX urological diseases, cardiovascular diseases and cancer.

XX Claim 2; Page 21-22; 24pp; English.

The invention relates to an isolated G-protein coupled receptor  
polypeptide, AXOR35, (and its homologues and variants) and its encoding  
polynucleotide (and its homologues, variants, complements and RNA  
equivalents). Also included are an anti-AXOR35 antibody, an AXOR35  
expression vector, producing a recombinant host cell by introducing the  
vector into a cell such that the host cell produces AXOR35, a membrane of  
the host cell expressing AXOR35, identifying/screening for agonists or  
antagonists of AXOR35 and inhibiting or promoting the function of  
lymphocytes, macrophages, eosinophils, or neutrophils in diseased tissue,  
by administering to the patient AXOR35 agonists or antagonists. The  
agonist or antagonist identified is useful for treating a disease such as  
asthma, or for inhibiting or promoting the function of lymphocytes.

macrophages, eosinophils, or neutrophils in diseased tissue such as an  
aethmatic lung. AXOR35 or polynucleotide is useful in diagnostic assays,  
for identifying compounds that are agonists or antagonists of AXOR35, as  
vaccines, or for treating infections (bacterial, fungal, protozoan or  
viral infections), transplant rejection, gastrointestinal disorders (such  
as gastric ulcer), inflammatory bowel diseases (such as Crohn's disease),  
irritable bowel syndrome, vomiting, inflammation (such as atopic  
dermatitis), allergy, autoimmune disorders (such as rheumatoid arthritis,  
psoriasis), urological diseases (such as urinary retention),  
cardiovascular diseases (such as myocardial infarction), hypotension,  
hypertension, pulmonary disorders (such as chronic obstructive pulmonary  
disease), cough, renal diseases (such as renal ischaemia),  
arteriosclerosis, atherosclerosis, psychotic and neurological disorders  
(such as migraine, anorexia, anxiety, schizophrenia), dyskinesias (such  
as Parkinson's disease), cancer, obesity, stroke, septic shock, graft  
versus host disease and osteoporosis. The present sequence is the cDNA  
encoding AXOR35

XX  
SQ Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;

Query Match 56.98; Score 669; DB 10; Length 1173;  
Best Local Similarity 74.21; Pred. No. 3.8e-206;  
Matches 875; Conservative 0; Mismatches 295; Indels 9; Gaps 2;

Qy 1 ATGTCGGAGTCTAACGGCACTGACGCTCTGCCACTGCTCAAGTCCCTTGGCATTT 60  
Db 1 ATGCCAGATCTAATAGCACAATCAATTTATCACTAGCACTCGTGTACTTTAGCATTT 60  
Qy 61 TTAATGTCCTGCTGCTTTTGTATTAACGATAGGCAATGCTGTGGTCATTTTAGCCCTT 120  
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Qy 361 CGTTATAGACACAGCACACTGGCATCTCGAAATTTGTTGCTCAAAATGGTGGCTGTTTGG 420  
Db 361 TCTTATAGACTCAACATCTGGGTCTTGAAGATTGTTACTCTGATGGTGGCGTGTGG 420  
Qy 421 ATACTGCTTTCTTGGTCAATTTGGCCCAATGATCTGGCTTGGGATTTCTGGAAAGACAGC 480  
Db 421 GTGCTGGCTTCTTAGTGAATGGGCCAATGATTTCTAGTTTTCAGAGTCTTGGAGGA--- 476  
Qy 481 ACCAACACAGGAGTGGAGCTGGCTTGGTGTGATGTTGCTGATGTTGCTCGCATCTCCATACA 540  
Db 477 --TGAAGGTAGTGAATGTGAACCTGGATTTTTCGGAATGGTATACATCTTGGCCATACA 534  
Qy 541 GCATTTCTGGAATTTCTGCTCCCTGTCTCTTGGTGGTCTATTTTCACTGATGACATTTAC 600  
Db 535 TCATTTCTGGAATTTCTGATCCCAAGTCACTTGTAGTGGCTTATTTCAACATGAATTTAT 594  
Qy 601 TGGAGCTGTGGAAGCGTGGAGTCTCAGTAGTGTCCTAGCCACGCTGGATTTCATCGCT 660  
Db 595 TGGAGCTGTGGAAGCGTGTATCTCAGTAGTGTCCTAGGAGCCATCTCGACTGACTGCT 654  
Qy 661 ACCTCTTCCAGGGGCACTGGACACTCAGCAGACTCGGTGGCTTGTAGGACAAAGTCTT 720  
Db 655 GTCTCTTCCAACTCTGTGGACACTCAATTCAGAGGTAGACTATCTTCAAGGAGATCTCTT 714  
Qy 721 CCTGGATTAAAGGAACCGCGCATCCCTTCTTCAATTCAGAAAGTCCACGAGGAAGAGCAGT 780

Db 715 TCTGCATCGACAGAGTCTCTGATCTCTTCAATTCAGAGAGACAGAGAGAGTAGT 774  
Qy 781 CTCTCGGTGCTTAAAGACTACATGAGGGTGTAGTATCATCCCTTCAAAGTGGGTTC 840  
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Db 835 TTCTCCAATCAGATCTGTAGCTTCCAAAGGGAACATGTTGAACGCTTAGAGCC 894  
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Qy 1021 TGGTACAGCATAGCCTTTTGGCTACAGTGTTCATTCATTCATTCCTTCTTCTATAC 1080  
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Qy 1141 CAGACACCTTC---ACAGACCCAGTCAATCTTCTTGA 1176  
Db 1135 CCTCTACCATCACAACACAGTCGGTCACTATCTTCTTAA 1173

RESULT 15  
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ID ADJ26922 standard; cDNA; 1173 BP.  
XX AC ADJ26922;  
XX AC AC (first entry)  
XX 20-MAY-2004 (first entry)  
XX Human endogenous orphan G-protein coupled receptor RUP7 cDNA.  
XX Human; G protein-coupled receptor; GPCR; dot-blot analysis;  
XX pharmaceutical agent; gene; ss.  
XX Homo sapiens.  
XX Key Location/Qualifiers  
XX CDS 1..1173  
XX /tag= a  
XX /product= "Human endogenous orphan GPCR protein"  
XX US2003175891-A1.  
XX PN 18-SEP-2003.  
XX PD 21-MAR-2003; 2003US-00393807.  
XX PP 20-NOV-1998; 98US-0109213P.  
XX PR 16-FEB-1999; 99US-0120416P.  
XX PR 26-FEB-1999; 99US-0121852P.  
XX PR 12-MAR-1999; 99US-0123946P.  
XX PR 12-MAR-1999; 99US-0123949P.  
XX PR 28-MAY-1999; 99US-0136436P.  
XX PR 28-MAY-1999; 99US-0136437P.  
XX PR 28-MAY-1999; 99US-0136439P.  
XX PR 28-MAY-1999; 99US-0136567P.  
XX PR 28-MAY-1999; 99US-0137127P.  
XX PR 28-MAY-1999; 99US-0137131P.  
XX PR 28-JUN-1999; 99US-0141448P.  
XX PR 28-SEP-1999; 99US-0156333P.  
XX PR 28-SEP-1999; 99US-0156555P.  
XX PR 29-SEP-1999; 99US-0156634P.



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PR 01-OCT-1999; 99US-0157281P.  
PR 01-OCT-1999; 99US-0157282P.  
PR 01-OCT-1999; 99US-0157293P.  
PR 01-OCT-1999; 99US-0157294P.  
PR 12-OCT-1999; 99US-00417044.  
PR 17-OCT-2002; 2002US-00272983.  
XX (CHEN/) CHEN R.  
PA (DANG/) DANG H T.  
PA (LIAN/) LIAN C W.  
PA (LINI/) LIN I.  
XX  
XX Chen R, Dang HT, Liaw CW, Lin I;  
XX  
XX WPI; 2003-898539/82.  
DR P-PSDB; ADJ26923.  
XX  
XX New human G protein-coupled receptor and its coding cDNA, useful for  
PT disease or disorder identification and/or selection, for screening of  
PT candidate compounds useful as pharmaceutical agents, and in research  
PT applications.  
XX  
XX Claim 25; SEQ ID NO 13; 53pp; English.  
XX  
XX The present invention relates to human endogenous orphan G protein-  
CC coupled receptor (GPCR) proteins and polynucleotides encoding such  
CC proteins. The cDNA sequence of the human G protein-coupled receptor  
CC (GPCR) is useful in making a probe for dot-blot analysis against tissue-  
CC mRNA and/or for RT-PCR identification of the expression of the receptor  
CC in tissue samples. GPCR sequences of the invention may be used in  
CC disease/disorder identification and/or selection, in screening of  
CC candidate compounds for use as pharmaceutical agents and in research  
CC settings. The present sequence is human endogenous orphan GPCR cDNA.  
XX  
XX Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;  
SQ  
Query Match 56.9%; Score 669; DB 11; Length 1173;  
Best Local Similarity 74.2%; Pred. No. 3.8e-206;  
Matches 875; Conservative 0; Mismatches 295; Indels 9; Gaps 2;  
Oy 1 ATGTCGGAGTCTACGGCACTGAGCGTCTTGCCACCTGCTGCTCAAGTCCCTTGCCATTT 60  
Db 1 ATGCCAGATACATAATAGCAACAATCAATTTATCACTAAGCACTCGGTGTACTTTAGCATTT 60  
Oy 61 TTAATGTCCTGCTGCTTTGCTATACGATGCAATGCTGCTGCTGCTGCTGCTGCTGCTTT 120  
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Db 121 GTGGTGGACAAACCTTAGACATCGAAGTAGTATTATTTTCTTAATTTGGCCATCTCT 180  
Oy 181 GACTTCTTGTTGGGTGTCATCTCCATTCCTCTGTACATCCCTCAACGCTGTTAACTGG 240  
Db 181 GACTTCTTGTTGGGTGTCATCTCCATTCCTCTGTACATCCCTCAACGCTGTTAACTGG 240  
Oy 241 AATTTTGGAAGTGGATCTGCATGTTTGGCTCACTACTGACTATCTTTTGGCAGACGA 300  
Db 241 GATTTTGGAAAGGAAATCTGTGATTTTGGCTCACTACTGACTATCTGTATGTACAGCA 300  
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Db 301 TCTGTATATACATTGCTCTCATCAGCTATGATCGATACCTGCTAGTCTCAATGCTGTG 360  
Oy 361 CGTTATAGACACAGCACTGGCATCTGTAATAATTTGTTGCTCAAAATGGTGGCTGTTGG 420  
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Search completed: August 5, 2005, 12:28:54  
Job time : 661 secs

Oy 481 ACCAACACAGAGGAGTCCGAGCCCTGGCTTTGTTACTGAGTGGTACATCTCCGCCATTACA 540  
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Oy 601 TGGAGCCTGTGGAAGCGTGGGAGTCTCAGTAGGTGCGCTAGCCAGCTGGGATTCATCGCT 660  
Db 595 TGGAGCCTGTGGAAGCGTGCATCTCAGTAGGTGCGCAAGCCATCTCGGACTGACTGCT 654  
Oy 661 ACCTTTCCAGGGGCACCTGGACACTCAGCGAGAACTGGGTTGGCTTGTAGACAAAGTCTT 720  
Db 655 GTCTCTTCCAAACATCTGTGGACACTCATTCAGAGGTAGACTATCTTCAAGGAGATCTCTT 714  
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Oy 841 TTCTGCCGATCAGAAAGCCAGTCTCTTCCAGAGAGACAGTGGAGCTTCTCAGAGGC 900  
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Oy 1141 CCAGCACCTTC---ACAGACCCAGTCAAGTATCTTCTTGA 1176  
Db 1135 CCTCTACCAACACACACAGTCGTCAGTATCTTCTTAA 1173

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: August 5, 2005, 09:19:14 ; Search time 5070 Seconds  
(without alignments)  
11239.316 Million cell updates/sec

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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9: gb\_pr.\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	670.6	57.0	1173	6 AX301763	Sequence
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7	669	56.9	1173	6 AX391860	Sequence
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22	669	56.9	1316	9 BC069136	Homo sapi
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26	623	53.0	1291	4 AB053300	Sus scrofa
27	616.8	52.4	1451	10 AF358858	Cavia por
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31	424.4	36.1	169144	9 AC090244	Homo sapi
32	424.4	36.1	184938	2 AP002476	Homo sapi
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38	167.8	14.3	1249	10 AF267538	Cavia por
39	158.4	13.5	1239	6 E39806	Novel guano
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ALIGNMENTS

RESULT 1	AF358860	1593 bp	mrna	linear	ROD 02-SEP-2001
LOCUS	AF358860				
DEFINITION	Rattus norvegicus histamine H4 receptor mRNA, complete cds.				
ACCESSION	AF358860				
VERSION	AF358860.1	GI:15420536			
KEYWORDS					
SOURCE	Rattus norvegicus (Norway rat)				
ORGANISM	Rattus norvegicus				
REFERENCE	1 (bases 1 to 1593)				
AUTHORS	Liu, C., Wilson, S., Kuei, C. and Lovenberg, T.W.				
TITLE	Comparison of human, mouse, rat, and guinea pig histamine H4 receptor suggests substantial species variation				
JOURNAL	Unpublished				
REFERENCE	2 (bases 1 to 1593)				
AUTHORS	Liu, C., Wilson, S., Kuei, C. and Lovenberg, T.W.				
TITLE	Direct Submission				
JOURNAL	Submitted (12-MAR-2001) Molecular Pharmacology, The R.W. Johnson Pharmaceutical Research Institute, 3210 Merryfield Row, San Diego, CA 92121, USA				

FEATURES	Location/Qualifiers
source	1..1593
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CDS	













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DEFINITION Sequence 1 from patent US 6613533.  
ACCESSION AR391860  
VERSION AR391860.1 GI:40115588  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1173)  
AUTHORS Behan, J. X., Hedrick, J. A., Laz, T. M., Monsma, F. J., Morse, K. L.,  
Unland, S. P., and Wang, S.  
TITLE Histamine receptor  
JOURNAL Patent: US 6613533-A 1 02-SEP-2003;  
FEATURES Location/Qualifiers  
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Query Match 56.9%; Score 669; DB 6; Length 1173;  
Best Local Similarity 74.2%; Pred. No. 9.4e-191;  
Matches 875; Conservative 0; Mismatches 295; Indels 9; Gaps 2;  
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DB 477 --TGAAGGTAGTGAATGTGAACCTGGAATTTTTCGGAATGGTACATCTTGGCCATCACA 534  
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DB 1135 CCTTACCATCACAAACAGTCGCTCAGTATCTTCTTAA 1173

RESULT 8  
LOCUS AX109119 1173 bp DNA linear PAT 30-APR-2001  
DEFINITION Sequence 1 from Patent WO0125432.  
ACCESSION AX109119  
VERSION AX109119.1 GI:13924093



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KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Behan, J.X., Hedrick, J.A., Laz, T.M., Monsma, F.J., Morse, K.L.,
            Umland, S. and Wang, S.
TITLE       Histamine receptor
JOURNAL     Patent: WO 0125432-A 1 12-APR-2001;
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FEATURES    Location/Qualifiers
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Best Local Similarity 74.2%; Pred. No. 9.4e-191;
Matches 875; Conservative 0; Mismatches 295; Indels 9; Gaps 2;

QY 1 ATGTCGGAGTCTAACGGCACTGACGCTTCCCACTGACTGCTCAAGTCCCTTGGCAATTT 60
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DEFINITION Sequence 1 from Patent EP1096009.
ACCESSION  AX139113
VERSION     AX139113.1 GI:14274791
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Homo sapiens
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Peter, B. and O'Reilly, M.A.
TITLE       G-protein coupled receptor-like polypeptide
JOURNAL     Patent: EP 1096009-A 1 02-MAY-2001;
            Pfizer Limited (GB); PFIZER INC. (US)
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Query Match      56.9%; Score 669; DB 6; Length 1173;
Best Local Similarity 74.2%; Pred. No. 9.4e-191;
Matches 875; Conservative 0; Mismatches 295; Indels 9; Gaps 2;

QY 1 ATGTCGGAGTCTAACGGCACTGACGCTTCCCACTGACTGCTCAAGTCCCTTGGCAATTT 60
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RESULT 10
BD015847
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
BD015847
Novel polypeptide.
BD015847
BD015847.1 GI:22556984
JP 2001211889-A/1.
Homo sapiens (human)
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ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1173)
AUTHORS Peter B. and Olaylee, M.A.
TITLE Novel polypeptide
JOURNAL Patent: JP 2001211889-A 1 07-AUG-2001;
PFIZER INC
COMMENT OS Homo sapiens (human)
PN JP 2001211889-A/1
PD 07-AUG-2001
PF 27-OCT-2000 JP 2000329359
PR 29-OCT-1999 GB 9925641:4, 20-APR-2000 GB 0009973:9 PI
BEAT PETER, MARK ANTONY OLAYLEE
PC C12N15/09, A61K38/00, A61K39/395, A61K48/00, A61P1/04,
PC A61P11/00,
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Hieble, P., Wilson, S., Bergsma, D.J. and Fitzgerald, L.R.  
Cloning, expression, and pharmacological characterization of a  
novel human histamine receptor  
Mol. Pharmacol. 59 (3), 434-441 (2001)  
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VERSION AF329449.1 GI:13876643
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Morse,K.L., Behan,J., Laz,T.M., West,R.E. Jr., Greenfeder,S.A.,
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Gustafson,E.L., Qiao,X., Wang,S., Hedrick,J.A., Greene,J., Bayne,M.
and Monsma,F.J. Jr.
Cloning and characterization of a novel human histamine receptor
J. Pharmacol. Exp. Ther. 296 (3), 1058-1066 (2001)
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MEDLINE 11181941
PUBMED
2 (bases 1 to 1173)
Monsma,F.J. Jr., Wang,S., Behan,J., Laz,T.M., Greene,J. and
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Direct Submission
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Research Institute, 2015 Galloping Hill Rd., Kenilworth, NJ 07033,
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1 (bases 1 to 1173)  
Nguyen, T., Shapiro, D.A., George, S.R., Setola, V., Lee, D.K.,  
Cheng, R., Rauser, L., Lee, S.P., Lynch, K.R., Roth, B.L. and  
O'Dowd, B.P.

Discovery of a novel member of the histamine receptor family  
Mol. Pharmacol. 59 (3), 427-433 (2001)  
21106319  
PUBMED 11179435

2 (bases 1 to 1173)  
Nguyen, T., George, S.R., Lee, D.K., Cheng, R., Lynch, K.R. and  
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Discovery of H4, a Novel Histamine Receptor  
Unpublished

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Nguyen, T., George, S.R., Lee, D.K., Cheng, R., Lynch, K.R. and  
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Direct Submission  
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KEYWORDS	histamine receptor H4; HRH4 gene.
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ORGANISM	Homo sapiens
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REFERENCE 1	O'Reilly, M.A.
AUTHORS	Identification of a histamine H4 receptor on human eosinophils -
TITLE	Role in eosinophil chemotaxis
JOURNAL	Unpublished
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AUTHORS	O'Reilly, M.A.
TITLE	Direct Submission
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	/mol_type="mRNA"
	/db_xref="taxon:9606"
	/cell_line="AML14.3D10"
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	/gene="HRH4"
CDS	1..1173
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	/codon_start=1
	/evidence=experimental
	/product="histamine receptor H4"
	/protein_id="CAC83493.1"
	/db_xref="GI:18152453"
	/db_xref="GOA:Q9H3N8"
	/db_xref="UniProt/Swiss-Prot:Q9H3N8"
	/translation="MPDNTSTNLSLSTRLVTLAPFMSLVAFALMGALNVILAFVVDK NLRHRSYFLALAIISDFVIGISIPLYLPHLPFDWDFKICIVFWLTDVLLCTASY YNILVSORYLSVNAVSYRQHTGVLLKI VTLMAVWVLAFLVNGPMILVBSWKDB GSECEPQPSSEVILAITSFLEFVLPVILVAFNNNIYMSLWKDRHLSRCQSHPLTA VSNICGHSFGRGLSRRLSLSASTEVASFHSERQRKSSLMFSRKNKNTIASKM GFSQSDSVLHOREVHELLRLAKSLAILLGVFVCMAPYSLFTVILVFSYSATG PKSVWYRIAPFLQWFNSFVNPLLYPLCHKRFQKFLKFCIKQPLPSQHSRSVSS"
ORIGIN	
Query Match	56.9%; Score 669; DB 9; Length 1173;
Best Local Similarity	74.3%; Pred. No. 9.4e-191;
Matches	875; Conservative 0; Mismatches 295; Indels 9; Gaps 2;
QY	1 ATGTCGAGTCTAACCGCACTGACGCTTGCCCACTGACTGCTCAAGTCCCTTTGGCATTT 60
DB	1 ATGCCAGATCTAATAGACAAATCAATTTATCACTAAGCACTCGTGTACTTTAGCATTT 60
QY	61 TTAATGTCCTGCTGCTTTTGTCTATAAGCATAGGCAATGCTGTGGTCACTTTTAGCCTTT 120

Search completed: August 5, 2005, 13:53:37

search completed: Aug  
Job time : 5077 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 5, 2005, 09:23:38 ; Search time 3693 Seconds  
(without alignments)  
12121.197 Million cell updates/sec

Title: US-10-626-126-6  
Perfect score: 1176  
Sequence: 1 atctcgagtgctaacggcac.....cccagtcagtatcttttga 1176

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST.\*

1: gb\_est1.\*  
2: gb\_est2.\*  
3: gb\_hic.\*  
4: gb\_est3.\*  
5: gb\_est4.\*  
6: gb\_est5.\*  
7: gb\_est6.\*  
8: gb\_gss1.\*  
9: gb\_gss2.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	437	37.2	839	5	EX643713	EX643713 DKFZp781C
2	420	35.7	704	7	CF147821	CF147821 AGENCOURT
3	253.2	21.5	721	7	CO959034	CO959034 AGENCOURT
4	133	11.3	853	6	CD326085	CD326085 AGENCOURT
5	131	11.1	672	6	CB555920	CB555920 AMGNNUC:U
6	129.4	11.0	732	7	CF147822	CF147822 AGENCOURT
7	115.6	9.8	684	9	CC481311	CC481311 CH240_309
8	95.8	8.1	643	1	AL848045	AL848045 AL848045
9	93.8	8.0	716	7	CN423054	CN423054 170004245
10	90.4	7.7	499	2	BF567596	BF567596 UI-R-B00-
11	89.2	7.6	921	9	CNS03296	AL224547 Tetraodon
12	84.2	7.2	1046	5	BQ950659	BQ950659 AGENCOURT
13	82.2	7.0	1136	3	BC019470	BC019470 Mus muscu
14	79.8	6.8	505	5	BQ837058	BQ837058 rf37e04.y
15	78.2	6.6	410	5	BQ836551	BQ836551 rf47c11.y
16	77.6	6.6	701	5	BX851226	BX851226 BX851226
17	77	6.5	523	4	BJ122942	BJ122942 BJ122942
18	77	6.5	562	4	BJ103964	BJ103964 BJ103964
19	77	6.5	565	6	CB385348	CB385348 OSTF021G5
20	77	6.5	566	4	BJ119403	BJ119403 BJ119403
21	77	6.5	582	4	BJ108530	BJ108530 BJ108530
22	77	6.5	633	4	BJ763892	BJ763892 BJ763892
23	76	6.5	557	4	BJ123503	BJ123503 BJ123503
24	75.4	6.4	258	2	AW654609	AW654609 104607 MA

C	25	75	6.4	597	4	BM355525	BM355525 rr26a12.Y
26	74	6.3	889	6	CB565881	CB565881 AGENCOURT	
27	72.6	6.2	700	7	CO138455	CO138455 EST833126	
28	72.6	6.2	754	5	BU468854	BU468854 603373878	
29	72.4	6.2	727	7	CR366545	CR366545 CR366545	
30	72.4	6.2	890	4	BI731453	BI731453 603354331	
31	71.2	6.1	842	7	CO403631	CO403631 AGENCOURT	
32	69.2	5.9	946	5	BQ068856	BQ068856 AGENCOURT	
33	69.2	5.9	1103	4	BM548665	BM548665 AGENCOURT	
34	68.4	5.8	628	5	BQ399940	BQ399940 NISC_mp06	
35	68.4	5.8	875	6	CA472422	CA472422 AGENCOURT	
36	67	5.7	281	2	BB592940	BB592940 BB592940	
37	67	5.7	463	1	AU199960	AU199960 AU199960	
38	67	5.7	602	1	AU207762	AU207762 AU207762	
39	67	5.7	663	6	BY728212	BY728212 BY728212	
40	66.4	5.6	398	1	AJ661967	AJ661967 AJ661967	
41	66.4	5.6	795	6	CD804122	CD804122 UI-M-GV0-	
42	66.4	5.6	3816	3	AK081248	Mus muscu	
43	65.8	5.6	434	6	CB758850	AMGNNUC:S	
44	65.8	5.6	653	6	BY727560	BY727560 BY727560	
45	64.4	5.5	1770	9	AY400784	Mus muscu	

#### ALIGNMENTS

RESULT 1  
BX643713  
LOCUS BX643713 839 bp mRNA linear EST 04-SEP-2003  
DEFINITION DKFZp781C0629 rl 781 (synonym: hlcc4) Homo sapiens cDNA clone  
ACCESSION BX643713  
VERSION BX643713  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 839)  
AUTHORS Lauber, J., Bahr, A., Mewes, H.W., Weil, B., Amid, C., Osanger, A.,  
Fobo, G., Han, M. and Wiemann, S.  
TITLE EST (Lauber, J., Bahr, A., Mewes, H.W., Weil, B., Amid, C., et al.)  
JOURNAL Unpublished (2003)  
COMMENT Contact: MIPS

MIPS  
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany  
This is the 5' sequence of the clone insert  
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer  
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;  
sequenced by Qiagen (Hilden/Germany) within the cDNA sequencing  
consortium of the German Genome Project.  
No sl sequence available.  
This clone (DKFZp781C0629) is available at the RZPD in Berlin.  
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059  
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES  
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/clone="DKFZp781C0629"  
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cDNA-collection"

#### ORIGIN

Query Match 37.2%; Score 437; DB 5; Length 839;  
Best Local Similarity 75.8%; Pred. No. 9.8e-120;  
Matches 569; Conservative 0; Mismatches 175; Indels 7; Gaps 2;  
Qy 1 ATGTCGGAGTCTAACGGCAGCTGCTTGGCCACTGACTGCTCAAGTCCCTTGGCATTT 60

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Db      96 ATCCGATACATAAGCAATCAATTTATCACTAGCACTCGTGTACTTTAGCAATTT 155
Qy      61 TTAATGTCCTGCTGCTTTGCTTATACGATAGCAATGCTGTGGTCAATTTAGCCTTT 120
Db      156 TTTATGTCCTTAGTAGCTTTTGTCTATAATGCTAGAAATGCTTGGTCAATTTAGCTTTT 215
Qy      121 GTAGCAGACAGAACCTTAGACATCGAAGTAATTTATTTTCTTAATTTGGCTATTCT 180
Db      216 GTGGTGACAAAAACCTTAGACATCGAAGTAGTATTATTTTCTTAATTTGGCCATCTCT 275
Qy      181 GACTTCTTCTGGGTGCTATCTCCATTCCTCTGTACATCCCTCACAGCTGTTTAACTGG 240
Db      276 GACTTCTTCTGGGTGCTATCTCCATTCCTTGTACATCCCTCACAGCTGTTTAACTGG 335
Qy      241 AATTTTGGAAAGTGAAATCTGCAATGCTTTTGGCTATTAATCTGACTATCTTTTGTGACAGCA 300
Db      336 GATTTTGGAAAGGAAATCTGTGATTTTGGCTCACTACTGACTATCTGTTATGTACAGCA 395
Qy      301 TCCGTCTACAGATTGTCCTCATCTAGCTAGCATGATACAGTACAGTTCAGAGCTGTG 360
Db      396 TCTGTATATACATGTCCTCATCTAGCTAGCTATGATGATGATGATGATGATGATGATGATG 455
Qy      361 CGTTATAGACACAGCACACTGGCATCTGAAATTTGCTCAAAATGCTGCTGCTGCTGCTGCTG 420
Db      456 TCTATAGAACTCAACATCTGGGTCTTGAAGATGCTTACTCTGATGCTGGCGCTTGG 515
Qy      421 ATACTGCTTCTTGGTCAATGCGCCAAATGATTTGCTGCTCAAAATGCTGCTGCTGCTGCTGCTG 480
Db      516 GTGTGGCTTCTTAGTGAATGGCCAAATGATTTAGTCTTCAAGATGCTTGAAGGATGAA 575
Qy      481 ACCAACACAGAGGAGTGGGCTGCTTCTTACTGAGTGTACATCTCCCTGCGCATTACA 540
Db      576 GGTAA-----GTGAATGTGAACCTGGATTTTTCGGAATGGTATACCTTGGCCATCACA 629
Qy      541 GCATTTCTTGAATTTCTGCTCCCTGCTCTCTTGGTGTCTATTTTCAAGTGTACAGATTTAC 600
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Qy      601 TGGAGCTGTGGAAAGCTGGAGTCTCAGTAGTGGCTAGCCAGCTGGAATTCATCGCT 660
Db      690 TGGAGCTGTGGAAAGCTGATCATCTCAGTAGGTGCGAAAGCCATCTCGGACTGACTGCT 749
Qy      661 ACCTTTCCAGGGGACATGGACATCCAGCAGACTGGGTGGCTGTGAGACAGTCTT 720
Db      750 GTCTCTTCCA-CATCTGTGGACATCATTTCAAGAGTGAATCTCTCAAGAGATCTCTT 808
Qy      721 CCTGGATTAAAGGAACCGACCGCATCCCTTC 751
Db      809 TCTGCATCGACAGAAAGTTCTCTGCATCCTTTC 839

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RESULT 2
CF147821 704 bp mRNA linear EST 25-JUL-2003
LOCUS AGNCOURT 14740195 NIH MGC 145 Homo sapiens cDNA clone
DEFINITION IMAGE.6971900 5', mRNA sequence.
ACCESSION CF147821
VERSION CF147821.1 GI:33244089
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 704)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
CONTACT: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgaapbe-r@mail.nih.gov

```

```

Tissue Procurement: GPCR Consortium
CDNA Library Preparation: GPCR Consortium
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: IRB102 row: b column: 07
High quality sequence stop: 685.
Location/Qualifiers
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/notes="Vector: pCDNA3.1; Site 1: varies by clone; Site 2:
varies by clone; ORFs were PCR-amplified and cloned into
pCDNA3.1 by the GPCR Consortium. Cloning sites vary by
clone and include the following: 5'-EcoRV-XmiI/XhoI-3',
5'-EcoRV-XmiI/NotI-3', EcoRV (TA cloned, non-directional).
For information about which gene each clones represents,
please visit our anonymous ftp site at
ftp://image.llnl.gov/image/rearrayed_plates/IRB1.preSV.dat
a Note: this is a NIH_MGC Library."

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## ORIGIN

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Query Match 35.7%; Score 420; DB 7; Length 704;
Best Local Similarity 76.5%; Pred. No. 1-2e-114;
Matches 543; Conservative 0; Mismatches 160; Indels 7; Gaps 2;
Qy 3 GTCGAGTCTAACGGCACTGACGCTCTTCCACTGACGTCTCAAGTCCCTTGGCAATTTT 62
Db 1 GCCAGATACCTAATAGCACAAATCAATTTATCACTAAGCACTCGTGTACTTTAGCAATTTT 60
Qy 63 AATGTCCTCTGCTGCTTTGCTATACGATAGCAATGCTGTGCTATTTTGGCTTTTGT 122
Db 61 TATGTCCTTAGTAGTCTTTTGTCTATAATGCTAGGAATGCTTTGCTCAATTTTGGCTTTTGT 120
Qy 123 AGCAGACAGAAAACCTTAGACATCGAAGTAATTTTCTTAATTTGGCTATTTCTGA 182
Db 121 GGTGACAAAAACCTTAGACATCGAAGTAGTATTTTCTTAACCTTGCCATCTCTGA 180
Qy 183 CTTCTTCTGGGTGTGATCTCCATTCCTCTGTACATCCCTCACAGCTGTTTAACTCGAA 242
Db 181 CTTCTTCTGGGTGTGATCTCCATTCCTCTGTACATCCCTCACAGCTGTTTAACTCGAA 240
Qy 243 TTTTGGAAAGTGGAGTCTGCAATGTTTGGCTCATTTACTGACTATCTTTTGTGCACAGATC 302
Db 241 TTTTGGAAAGAAATCTGTATTTTGGCTCACTACTGACTATCTGTATGTACAGATC 300
Qy 303 CGTCTACAGTATTTGCTCTCATTTAGCTACGATACGATACAGTCTTCAACGCTGTGCG 362
Db 301 TGTATATAACATTTGCTCTCATCAGCTATGATGATGATGATGATGATGATGATGATGATG 360
Qy 363 TTATAGACACAGCACTCTGGCATCTGAAATTTGTTGCTCAAAATGCTGCTGCTGTTTGGAT 422
Db 361 TTATAGAACTCAACATCTGGGTCTTGAAGATGTTTACTCTGATGCTGGCGCTTGGGT 420
Qy 423 ACTGGCTTTCTTGGTCAATGCGCCAAATGTTCTGGCTTCGGATTTCTTGGAGAACAGCAC 482
Db 421 GCTGGCTTTCTTGTAGTAATGGCCAAATGATTTCTAGTTTCAAGATCTTTGGAAAGGA----- 474
Qy 483 CAACACAGAGAGTGGCAGGCTGGCTTTTGTACTGTAGTGGGTGTACTCTCGCCATTACAGC 542
Db 475 TGAAGGTAGTGAATGTGAACCTGGATTTTTCGGAATGTTGTACATCTTGCCATCACATC 534
Qy 543 ATTCTTGGAAATTCCTGCTCTCTCTGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 602
Db 535 ATTCTTGGAAATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 594

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## FEATURES

## Source

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Qy 603 GAGCTGTGGAGCGTGGAGTCTCAGTAGTGCCTAGCCACCGCTGATTCATCGCTAC 662
Db 595 GAGCTGTGGAGCGTGGAGTCTCAGTAGTGCCTAGCCACCGCTGATTCATCGCTAC 654
Qy 663 CTCCTCCAGGGGCACTGACACTCAGCAGAACTGGGTGGCTTGTAGGA 712
Db 655 CTCCTCCA-CATCTGTGGACACTATTCAGAGGTAGACTATCTTTCAGGA 703

RESULT 3
LOCUS CO959034
DEFINITION AGNCOURT_30842625 NIH_MGC_146 Homo sapiens cDNA clone
IMAGE:7389774 5', mRNA sequence.
ACCESSION CO959034
VERSION CO959034.1 GI:51323616
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 721)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-remail.nih.gov
Tissue Procurement: Guthrie cDNA Resource Center
cDNA Library Preparation: Guthrie cDNA Resource Center
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: IRB18 row: a column: 04
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High quality sequence stop: 328.
Location/Qualifiers
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/note="Vector: pCDNA3.1; Site_1: multiple; Site_2:
multiple; ORF's were PCR-amplified (from IMAGE clones or
from commercially available cDNA libraries) and cloned by
the Guthrie cDNA Resource Center (www.guthrie.org/cDNA)
into pCDNA3.1. For specific information on cloning sites
(which vary by clone), please refer to the Guthrie
website, using the Guthrie ID given in the file
ftp://image.llnl.gov/image/rearrayed_plates/IRBP.presv.dat
a. Note: this is a NIH_MGC Library."

ORIGIN
Query Match 21.5%; Score 253.2; DB 7; Length 721;
Best Local Similarity 77.7%; Pred. No. 2.2e-64;
Matches 306; Conservative 0; Mismatches '88; Indels 0; Gaps 0;

Qy 1 ATGTCGGAGTCTAAGCGCACTGAGTCTTGGCACTGCTCAAGTCCCTGGCAATT 60
Db 22 ATGCAGATACATAATAGCACAAATCAATTTATCAATAGCACTCGGTACTTTAGCA 81
Qy 61 TTAATGTCCTGCTGCTTTGCTATAACGATAGCAATGCTGTGCTATTTAGCCCTT 120
Db 82 TTTATGCTCTAGTAGCTTTTGCTATATATGCTAGGAATGCTTTGGTCAATTTAGCT 141
Qy 121 GTAGCAGACAGAAACCTTAGACATCGAAGTAATTTATTTTCTTAAATTTGGCTATTCT 180

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Db 142 GTGGTGACAAAAACCTTAGACATCGAAGTAGTTATTTTCTTAACCTGGCCATCTCT 201
Qy 181 GACTTCTTCGGGGGTGTCATCTCCATTCTCTGTACATCCCTCACACGCTGTTTAACTGG 240
Db 202 GACTTCTTCGGGGGTGTCATCTCCATTCTCTGTACATCCCTCACACGCTGTTTAACTGG 261
Qy 241 AATTTTGGAAAGTGAATCTGCATGTTTTGGTCTCAATTAAGTCTATCTTTTGTGCACAGA 300
Db 262 GATTTTGGAAAGGAAATCTGTGTATTTTGGCTCACTACTGACTATCTCTTATGTACCGCA 321
Qy 301 TCCGCTCTACAGTATTGCTCCTCATTTAGCTACCATCGATACCATGATTTTCAACGCTGTG 360
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Qy 361 CGTTATAGAGCACAGCACACTGGCATCTCTGAAAA 394
Db 382 TCTTATGGAACGCAAAAAACGGGGGCTGAAGA 415

RESULT 4
LOCUS CD326085
DEFINITION AGNCOURT_14163426 NICH_XGC_Eyel Xenopus laevis cDNA clone
IMAGE:6949081 5', mRNA sequence.
ACCESSION CD326085
VERSION CD326085.1 GI:31090416
KEYWORDS EST.
SOURCE Xenopus laevis (African clawed frog)
ORGANISM Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
Xenopodinae; Xenopus; Xenopus.
REFERENCE 1 (bases 1 to 853)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-remail.nih.gov
Tissue Procurement:
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM14564 row: f column: 24
High quality sequence stop: 707.
Location/Qualifiers
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/clone="IMAGE:6949081"
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/clone_lib="NICH_XGC_Eyel"
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Site_2: SalI; Cloned unidirectionally. Primer: Oligo dr.
Average insert size 2.3 kb. Constructed by Life
Technologies. Note: This is a Xenopus Gene Collection
(XGC) library."

ORIGIN
Query Match 11.3%; Score 133; DB 6; Length 853;
Best Local Similarity 59.3%; Pred. No. 3.7e-28;
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Qy 46 GTCCCTTGGCAATTTTAAATGCTGCTTGTCTATTAACGATAGGAATGCTGTG 105

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Db 382 GTCTTCCTGCTGTCCTAGTGGGGTCTCTCATAGTTAGCACCGTGTCTGGGAATGCCCTG 441
Qy 106 GTCAATTTAGCCTTTGTAGCAGACAGAAACCTTAGACATCGAAGTAATATTTTCTT 165
Db 442 GTCATGCTGCTTTGTGTGGACTCCAGCCTCCGAAACCCAGAAATATTTCTTCTCTC 501
Qy 166 AATTTGGCTATTTCTGACTTCTTCTGCTGGTGTATCTCCATTCCTCTGTACATCCCTCAC 225
Db 502 AACTGGCTATCTCAGATTTCTTTGTAGTGCCCTGTGCACTCCCTCTGTATGTGCCATAC 561
Qy 226 ACGCTGTT---AACTGGAAATTTGGAAAGTGAATCTGCAATGTTTGGCTCATTTACTGAC 282
Db 562 GTACTGACTGGCAGATGGAGCTTTGGCAGGAGCGTTTGCAAACTGTGGCTGTTCTGAT 621
Qy 283 TATCTTTTGTGCACAGATCGGCTACAGTATGTCTCTCATTAGCTAGGATCGATACAG 342
Db 622 TATCTGCTCTGCACCTCGTCCGTGTTCAACATCGTGTCTCATCAGCTACGACAGGTTTATC 681
Qy 343 TCAGTTTCAAAACGCTGTGGTATTATAGACACAGCACACTGGCATCTCGTGAATAATTTGTTGCT 402
Db 682 TCTGTGACCCGGCTGTGATTCAGTACCGAGCTCAGCAGAGTAACAGCCGCGATGCACTTTG 741
Qy 403 CAAATGGTGGCTGTTTGGACTACTGGCTTCTTGGTCAATGGCCCAATGATCT 455
Db 742 AAAATGACCATGGTGTGATCTTGGCTTCTCTATATGACCCAGCCATTAT 794

RESULT 5
CB556920
LOCUS
DEFINITION
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  urgp1-00001-d6 5', mRNA sequence.
ACCESSION
  CB556920
VERSION
  CB556920.1 GI:29496320
KEYWORDS
  EST.
SOURCE
  Rattus norvegicus (Norway rat)
ORGANISM
  Rattus norvegicus
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
  Rattus.
REFERENCE
  1 (bases 1 to 672)
  Angen EST Program.
  Angen Rat EST Program
  Unpublished (2003)
  Contact: Dan Fitzpatrick
  Angen, Inc
  One Angen Center Drive, Thousand Oaks, CA 91320-1799, USA
  Tel: 805 447-4881
  Plate: 00001 row: d column: 6.
  Location/Qualifiers
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      /clone="urgp1-00001-d6"
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      /note="Vector: pSPORn1; Rat GPCR library rearrayed
      internal pSPOR vector"

FEATURES
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      /organism="Rattus norvegicus"
      /mol_type="mRNA"
      /db_xref="taxon:10116"
      /clone="urgp1-00001-d6"
      /clone_lib="urgp1 (14349)"
      /note="Vector: pSPORn1; Rat GPCR library rearrayed
      internal pSPOR vector"

ORIGIN
  Query Match 11.1%; Score 131; DB 6; Length 672;
  Best Local Similarity 58.7%; Pred. No. 1.4e-27;
  Matches 246; Conservative 0; Mismatches 170; Indels 3; Gaps 1;

Qy 51 CTTGGCAATTTTAAATGCTGCTGCTTTTGGCTATAACGATAGCAATGCTGGTCAAT 110
Db 226 CTTGGCTGCTCATGCGCTGCTCATGCTGGCCACAGTACTGGGCAACGCGCTGGTCAAT 285
Qy 111 TTTAGCTTTTGTAGCAGACAGAAACCTTAGACATCGAGTAATATTTTCTTAATTT 170
Db 286 GCTCGCTTTGTGGCGAATTCGAGCTCCGACCCAGAACAACTTCTTCTGCTCAACCT 345
Qy 171 GGCTATTCTGACTTCTTCTGCTGGGTGTCATCTCCATTCCTCTGTACATCCCTCACAGCT 230
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Db 346 CGCATCTCGACTTCTCTGTGGTGCCTTCTGCATCCCATTTGTAGTACCTATGTGCT 405
Qy 231 GTTTAAAC---TGAATTTTGGAAAGTGAATCTGCATGTTTGTGCTCATTAAGTATCT 287
Db 406 GACCGGCGTGTGACCTTCGGCGGGGCTCTGCAAGCTGTGGCTGGTGTAGACTACCT 465
Qy 288 TTTGTGCACAGCATCCGCTTACAGTATTTGCTCTCATTAGCTACGATCGATACAGTCAGT 347
Db 466 ACTGTGTGCTCTCTCGTCTTCAACATCGTACTCATCAGCTATGACCGATTTCTGTGCT 525
Qy 348 TTCAAACGCTGTGGTATTATAGACACAGCACACTGGCATCTGAAATTTGTTGCTCAAT 407
Db 526 CATCTGAGCTGTCTCTTACAGGCCAGAGGGGGACACAGAGCGGCGCTTCGGAAGAT 585
Qy 408 GGTGGCTGTTTGGATCTGCTTTTCTGTGTCATATGCCCCAATGATTTGCTTGGATT 466
Db 586 GGCACCTGGTGGGTGCTGGCTTCTGCTGTATGGGCTGCCATCTGAGTTGGAGT 644

RESULT 6
CF147822
LOCUS
DEFINITION
  AGENCOURT 14740187 NIH MGC 145 Homo sapiens cDNA clone
  IMAGE:6971899 5', mRNA sequence.
ACCESSION
  CF147822
VERSION
  CF147822.1 GI:3244090
KEYWORDS
  EST.
SOURCE
  Homo sapiens (human)
ORGANISM
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1 (bases 1 to 732)
  NIH-MGC http://mgi.nci.nih.gov/.
  National Institutes of Health, Mammalian Gene Collection (MGC)
  Unpublished (1999)
  Contact: Daniela S. Gerhard, Ph.D.
  Office of Cancer Genomics / NIH
  National Cancer Institute / NIH
  Bldg. 31 Rm10A07 Bethesda, MD 20892
  Email: cgapbs-x@mail.nih.gov
  Tissue Procurement: GPCR Consortium
  cDNA Library Preparation: GPCR Consortium
  cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
  DNA Sequencing by: Agencourt Bioscience Corporation
  Clone distribution: MGC clone distribution information can be
  found through the I.M.A.G.E. Consortium/LLNL at:
  http://image.llnl.gov
  Plate: IRBI02 row: b column: 06
  High quality sequence stop: 610.
  Location/Qualifiers
    1..732
      /organism="Homo sapiens"
      /mol_type="mRNA"
      /db_xref="taxon:9606"
      /clone="IMAGE:6971899"
      /tissue_type="mixed"
      /lab_host="DH10B"
      /clone_lib="NIH_MGC_145"
      /note="Vector: pCDNA3.1; Site 1: varies by clone; Site 2:
      varies by clone; ORFs were PCR-amplified and cloned into
      pCDNA3.1 by the GPCR Consortium. Cloning sites vary by
      clone and include the following: 5'-EcoRV-XmnI/XhoI-3',
      5'-EcoRV-XmnI/NotI-3', EcoRV (TA cloned, non-directional).
      For information about which gene each clone represents,
      please visit our anonymous ftp site at
      ftp://image.llnl.gov/image/rearrayed_plates/IRBI.presv.dat
      a Note: this is a NIH_MGC Library."

FEATURES
  source
    1..732
      /organism="Homo sapiens"
      /mol_type="mRNA"
      /db_xref="taxon:9606"
      /clone="IMAGE:6971899"
      /tissue_type="mixed"
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      /clone_lib="NIH_MGC_145"
      /note="Vector: pCDNA3.1; Site 1: varies by clone; Site 2:
      varies by clone; ORFs were PCR-amplified and cloned into
      pCDNA3.1 by the GPCR Consortium. Cloning sites vary by
      clone and include the following: 5'-EcoRV-XmnI/XhoI-3',
      5'-EcoRV-XmnI/NotI-3', EcoRV (TA cloned, non-directional).
      For information about which gene each clone represents,
      please visit our anonymous ftp site at
      ftp://image.llnl.gov/image/rearrayed_plates/IRBI.presv.dat
      a Note: this is a NIH_MGC Library."

ORIGIN
  Query Match 11.0%; Score 129.4; DB 7; Length 732;
  Best Local Similarity 57.0%; Pred. No. 4.3e-27;
  Matches 257; Conservative 0; Mismatches 191; Indels 3; Gaps 1;
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Qy 53 TGGCATTTTAAATGTCCTGCTGCTTTTGTCTATAAGATAGGCAATGCTGTGTCATTT 112
|||
Db 126 TGGCGCGCTCATGGCGCTGCTCATGCTGGCCAGCTGCTGGCAACGCGTGTGTCATGC 185
|||
Qy 113 TAGCCTTTGTAGCAGACGAACTTACATCGAAGTAATATTTTCTTAATTTGG 172
|||
Db 186 TCGCCTTGTGGCGAGCTCGAGCCTTCGACCCAGAACAACTTCTTCTGCTCAACCTCG 245
|||
Qy 173 CTATTTCTGACTTCTTGTGGGTGTCATCTCCATTTCTCTGTACATCCCTCACAGCTG- 231
|||
Db 246 CCAITCTCGACTTCTTGTGGGCTTCTGCATCCCACTGTATGATACCTACGTGCTGA 305
|||
Qy 232 -TTTAATGAAATTTGGAAAGTGAATCTGCATGTTTGTGCTCATTAAGTATCTTT 289
|||
Db 306 CAGGCCGTGGACCTTCGGCCGGGCGCTCTGCAAGCTGTGGCTGTGTGACTACCTGC 365
|||
Qy 290 TGTGCACAGCATCGCTTACAGTATGTCCTCATTAAGTACGATGATACAGTCACTTT 349
|||
Db 366 TGTGCACCTCTCTGCTTCAACATGCTGCTCATCAGCTAGCAGCGCTTCTGCTGGTCA 425
|||
Qy 350 CAAACGCTGTGCGTTATAGACACACAGCACACTGGCATCTCTGAAAATTTGCTCAAAATGG 409
|||
Db 426 CCGAGCGTCTCATACCGGCCACAGAGGTGACACGGCGCGGAGTGGCGAATGC 485
|||
Qy 410 TGGCTGTTTGATGACTGCTTCTTGTGTCATGTCATGTCGCTTGTGCTTGTGCTT 469
|||
Db 486 TGTGCTGTGGTGTGCTGCTTCTGCTGTACGACAGCAGCATCTGAGCTGGAGTACC 545
|||
Qy 470 GGAAGACACACCAACACAGAGAGTGGCA 500
|||
Db 546 TGTCCGGGGCAGCTCCATCCCGAGGGCCA 576
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RESULT 7
CC481311
LOCUS CH240_309C10.T7 CHORI-240 Bos taurus genomic clone CH240_309C10,
genomic survey sequence.
CC481311
CC481311.1 GI:31760574
GSS.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos
1 (bases 1 to 684)
Holt,R., Stott,J., Yang,G., Barber,S., Smalley,D., Prabhu,A.-L.,
Teal,M., Cloutier,A., Lee,D., Gryn,N., Olson,T., Mayo,M.,
Butterfield,Y., Kirkpatrick,R., Liu,J., Guin,R., Chan,A., Chiu,R.,
Mathewson,C., Wye,N., Masson,A., Brown-John,M., Jones,S.,
Schein,J., Warra,M., de Jong,P., McWilliam,S., Barris,W.,
Dalrymple,B.P. and Tellam,R.
Bovine BAC End Sequences from Library CHORI-240, PLATES 294 to 398
Unpublished (2003)
Other GSSs: CH240_309C10.TARBAC13P2
Contact: Rob Holt
Sequencing
The British Columbia Cancer Agency Genome Science Centre
600 W. 10th Ave, Vancouver, British Columbia, Canada V5Z 4E6
Tel: 604-877-6085
Fax: 604-877-6276
Email: rholt@bcsc.ca
Clones are derived from the bovine BAC library CHORI-240
(http://www.chori.org/bacpac/bovine240.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@gmail.com).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/ordering/information.htm). This work
was undertaken as part of the International Bovine BAC Mapping
Consortium (IBBMC) by CSIRO Livestock Industries, Australia and the
British Columbia Genome Sciences Centre, Canada.
Plate: 309 row: C column: 10
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Seq primer: T7
Class: BAC ends.
Location/Qualifiers
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/mol_type="genomic DNA"
/strain="breed: Hereford"
/db_xref="taxon:9913"
/clone="CH240_309C10"
/sex="Male"
/cell_type="Blood"
/clone_lib="CHORI-240"
/notes="vector: pTARBAC1.3; Site 1: MboI; Site 2: MboI;
Hereford bull L1 Domino 99375; CHORI-240 Bovine BAC
library (Male) produced by Pieter de Jong"

ORIGIN
Query Match 9.8%; Score 115.6; DB 9; Length 684;
Best Local Similarity 70.6%; Pred. No. 6e-23;
Matches 154; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

Qy 150 TAATTAATTTTCTTAATTTGGCTATTCTGACTTCTTCTGCTGGTGTCTATCTCCATCC 209
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Db 260 TACGTGCTATATTGTTAACTTTCATTTTTCGCCCATGCAGGTATGATCTCCATCC 319
|||
Qy 210 TCTGTACATCCCTCACAGCTGTTTAACTGGAATTTTGGAGTGGAAATCTGCATGTTT 269
|||
Db 320 TTTATTATCCCTCACAGCTCTTCAACTGGAGTTTGAATAAATTAACATTTGTGCTTTTG 379
|||
Qy 270 GCTCATTTACTGACTATCTTTTGTGCACAGCATCGCTACAGTATTGCTTCATAGCTA 329
|||
Db 380 GCTCAGTACTGACTATCTTTTGTGTACAGCATCTGTGTATACATCTGACTCATCAGCTT 439
|||
Qy 330 CGATCGATACAGTCAGTCTTCAACAGCTGTGCGTTATA 367
|||
Db 440 TGATCGATATCAGTCAGTCTCCAATGCTGTAACTCAA 477
|||

RESULT 8
AL848045
LOCUS AL848045 XGC-egg Xenopus tropicalis cDNA clone TEGG022122 5', mRNA
DEFINITION AL848045.2 GI:38559584
ACCESSION AL848045
VERSION AL848045.2
KEYWORDS EST.
SOURCE Xenopus tropicalis (western clawed frog)
ORGANISM Xenopus tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
Xenopodinae; Xenopus; Silurana.
1 (bases 1 to 643)
Croning,M.D.R., Ashurst,J.L., Taylor,R., Zorn,A.M. and Rogers,J.
Sanger Xenopus tropicalis EST project 2001 (11_2003)
Unpublished (2003)
On Sep 15, 2002 this sequence version replaced gi:22868310.
Contact: Taylor R
Sanger Institute
Hinxtion, Cambridgeshire, CB10 1SA, UK
Email: tropesanger.ac.uk
Sanger Xenopus tropicalis EST project 2001
TROPICALIS_SEQUENCE ID: TEGG022122.plkSP6
Sequencing primer: SP6
This sequence is from a Xenopus Gene Collection (XGC) library
constructed by Aaron M. Zorn.
cDNA was oligo dT primed from 5'ug of poly A+ RNA from egg.
ECORI-NotI cut cDNA was then ligated into pCSI07 with EORI at the
5' end and NotI at the 3' end.
Vector: pCSI07; Site 1: EORI; Site 2: NotI
Host: Escherichia coli XL1-blue.
Location/Qualifiers
1..643
/organism="Xenopus tropicalis"

FEATURES
source
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/mol type="mRNA"
/db xref="taxon:8364"
/clone="FEgg022122"
/dev stage="egg"
/lab host="Escherichia coli XL1-blue"
/clone lib="XGC-egg"
/notes="Vector: pCS107; Site 1: EcoRI; Site 2: NotI; cDNA
was oligo dT primed from 5ug of poly A+ RNA from egg.
EcoRI-NotI cut cDNA was then ligated into pCS107 with
EcoRI at the 5' end and NotI at the 3' end"

ORIGIN
Query Match      8.1%; Score 95.8; DB 1; Length 643;
Best Local Similarity 55.1%; Pred. No. 5.4e-17;
Matches 234; Conservative 0; Mismatches 182; Indels 9; Gaps 2;

QY 193 GGTGTCATCTCCATTCCTCTGTATACATCCCTCACACGCTGTTT---AACTGGAAATTTTGGG 249
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DB 83 GGTGATTCCTGCATCCCACTCTATATCCCTATGTGCTGACTGGCCAGTGGAAATTTTGGG 142

QY 250 AGTGGAACTCGATGTTTGGCTCACTACTGATCTATCTTTTGTGCAAGCATCGTCTAC 309
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 143 AAAGGCTTGTGCAAGTTGTGGCTAGTAATGGACTACCTTTTATGCACTGCTTCAGTTTTT 202

QY 310 AGTATTGCTCTATTAGCTAGTACGATACAGTCAGTTCACACGCTGTGCGTTATAGA 369
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 203 AATATTGCTCTATCAGCTATGACAGGTTCTATCTCAGTCACTAAAGCGGTGCTCTACAGA 262

QY 370 GCACAGCACACTGGCATCTCCGAAATTTGCTCAAAATGGTGGCTGTTTGGATCTGGCT 429
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 263 GCACAGAAAGAAATGACAGAAATGCAAGTGTAAATGCTATTGTTGGTGGCAGCC 322

QY 430 TTCTTGCTCAATGGCCCAATGATTCCTGGCTCGGA-----TTCTTGGAAAGACAGACC 483
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 323 TTTCTTCTATGCGCCAGCCATCATCACTGGGAATACATTCGAAGAATCTATCTTA 382

QY 484 AACACAGAGAGTGGAGCTGGCTGTTGTTACTGAGTGGTACATCTCGCCATTCACAGA 543
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 383 CCAGAGGGGAATGTTATGTAGAAATCTACTACAACTGGTATTTTCTGATGATAGCTTCC 442

QY 544 TTCTTGGAAATCTCTGCTCCCTGCTCTGTTGGTGTCTATTTCAGTGTACAGATTTACTGG 603
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 443 ACAATAGAAATTTCTTACTCCATTCATCAGTGTACCTATTTCAATCTAAGCATCTACATT 502

QY 604 AGCT 608
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DB 503 AACAT 507

RESULT 9
CN423054
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J.,
Li, Y., Xu, C., Fang, R., Guebler, K., Rao, M.S., Mandalam, R.,
Lebkowski, J. and Stanton, L.W.
Transcriptome characterization elucidates signaling networks that
control human ES cell growth and differentiation
Nat. Biotechnol. 22 (6), 707-716 (2004)
Contact: Brandenberger R
Regenerative Medicine
Garon Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760

Email: rbrandenberger@eron.com
Insert Length: 716 Std Error: 0.00.
Location/Qualifiers
1..716
/organism="Homo sapiens"
/mol type="mRNA"
/db xref="taxon:9606"
/tissue_type="embryonic stem cells, cell lines H1, H7, and
H9"
/clone lib="GRN ES"
/notes="oligo dT primed, full-length enriched cDNA library
from undifferentiated hES cell lines H1 (p32), H7 (p29),
and H9 (p26) maintained in feeder-free conditions"

FEATURES
source
1..716
Email: rbrandenberger@eron.com
Insert Length: 716 Std Error: 0.00.
Location/Qualifiers
1..716
/organism="Homo sapiens"
/mol type="mRNA"
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/tissue_type="embryonic stem cells, cell lines H1, H7, and
H9"
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/notes="oligo dT primed, full-length enriched cDNA library
from undifferentiated hES cell lines H1 (p32), H7 (p29),
and H9 (p26) maintained in feeder-free conditions"

ORIGIN
Query Match      8.0%; Score 93.8; DB 7; Length 716;
Best Local Similarity 53.9%; Pred. No. 2.3e-16;
Matches 241; Conservative 0; Mismatches 197; Indels 9; Gaps 2;

QY 192 GGTGTCATCTCCATTCCTCTGTATACATCCCTCACACGCTG---TTTAACTGGAAATTTGG 248
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 200 GGGCGCTTCTGTCATCCCACTGTATGATACCTACGCTGCTGACAGGCGCTGGACCTTCGG 259

QY 249 AAGTGGAACTCGATGTTTGGCTCATTTACTGATCTTTTGTGCAAGCATCCGCTA 308
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 260 CCGGGGCTCTGCAAGCTGTGGCTGTAGTGGACTCTGTGACCTCTCTCTGCTT 319

QY 309 CAGTATTGCTCTATTAGCTACATCGATACCATACAGTTCAGTTTCAAAAGCTGTGGCTTATAG 368
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DB 320 CAACATCGTGTCTCATCAGCTACGACCGTTCCTGTCGGTCCACCGAGCGGTCTCATACCG 379

QY 369 AGCACAGCACACTGGCATCTCTGAAATTTGTTGCTCAAAATGGTGGCTGTTTGGTACTGGC 428
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 380 GGGCCAGCAGGGTGACACGCGCGGCGAGTGCAGAAAGATGCTGCTGTGGGTGGTGGC 439

QY 429 TTTCTTGGTCAATGGCCCAATGTTCTGGCTTCGGA-----TTCTTGGAAAGAACAGCAC 482
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 440 CTTCTGCTGTAGGACACCGCATCTGAGTGGAGTACTCTCGGGGGCAGCTCAT 499

QY 483 CAACACAGAGAGTGGAGCTGGCTTGTGTTTGTAGTGTGATATCTCTGCCATTCACAGC 542
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 500 CCGGAGGGCCACTGCTATGCCAGTCTTCTACAACTGCTACTTCTCATCAGGCTTC 559

QY 543 ATTCTTGGAAATCTCTGCTCTCTCTGTTGGTGTCTATTTCAGTGTACAGATTTTACTG 602
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 560 CACCTTGGAGTTCTTTACGCCCTTCTCTCAGGTCACCTTCTTTAACTCAGCATCTACCT 619

QY 603 GAGCTGTGGAAGCTGGAGTCTCAG 629
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DB 620 GAACATCCAGAGGGCACCCTCCG 646

RESULT 10
BF567596
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 499)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
JOURNAL
MEDLINE
PUBMED
8889548
Contact: Soares, MB

```



## Coordinated Laboratory for Computational Genomics

University of Iowa  
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA  
Tel: 319 335 8250  
Fax: 319 335 9565

Email: bento-soares@uiowa.edu  
cDNA Library Preparation: M.B. Soares Lab Clone distribution:  
clones will be available through Research Genetics (www.reagen.com)  
This clone is also available through the I.M.A.G.E. Consortium at  
LNL (info@image.lnl.gov). IMAGE ID= 1796445  
Seq primer: M13 Forward.

## FEATURES

Location/Qualifiers

source

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1..499
/organism="Rattus norvegicus"
/mol_type="mRNA"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-B00-agr-c-06-0-UI"
/dev_stage="adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="UI-R-B00"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; The library
(UI-R-B00) is a subtracted library derived from a mixture
of the following tissues: thalamus, cerebellum,
hypothalamus, medulla, pons, midbrain, cerebral
corpus striatum and hippocampus. For a detailed
description of the library from which this clone was
derived, please visit our web site at
rateest.eng.uiowa.edu. The subtraction has been previously
described in (Bonaldo, Lennon and Soares, Genome Research
6:791-806, 1996)"
```

## ORIGIN

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Query Match      7.7%; Score 90.4; DB 2; Length 499;
Best Local Similarity 53.8%; Pred. No. 2.1e-15;
Matches 234; Conservative 0; Mismatches 192; Indels 9; Gaps 2;

Qy 192 GGGTGTCTATCCATCTCTGTACATCCCTCACACGCTGTTTAAAC---TGGAAATTTGG 248
Db 58 GGGTGGCTTCTGCATCCCATTTGATGACCTATGCTGACCGCGCTTGGACCTTCGG 117

Qy 249 AAGTGGATCTGCATGTTTGGCTCATCTACTGATCTCTTTTGTGCACGATCCGTCCTA 308
Db 118 CCGGGGCTCTGCAGCTGTGGCTGGTGGTAGACTACTGCTGTGCTCTCTCGGTCTT 177

Qy 309 CAGTATTGCTCTATTAGTACGATCGATACCGATCTCAGTTTCAAACGCTGTGCGTTATAG 368
Db 178 CAACATGCTACTCATCAGCTATGACCGATTCCTGTCTAGTCACTCGAGCTGTCTCTACAG 237

Qy 369 AGCAGACACTGGCATCTCTGAAATTTGTTGCTCAAAATGGTGGCTGTTTGGATATGGC 428
Db 238 GGCCACAGCGGGGACAGACGCGGGCTTTCGGAAGATGCACTGTGTGGGTGCTGC 297

Qy 429 TTTCTTGGTCAATGGCCCAATGATTCTGGCTTCGGA-----TTCTTGGAAAGAACAGC 482
Db 298 CTTCTCTGTGTATGGGCGCTGCATCTCGAGTTGGGAGTACCTGTCTGGTGGCAGTTCCAT 357

Qy 483 CAACACAGAGAGTGCAGGCTGGCTTGTGTACTGAGTGGTACATCTCTCGCCATTACAGC 542
Db 358 CCCCAGGGCCACTGTGATGCTGAGTCTTTCTTCAAACTGGTACTTCTTCATCGGNGCTC 417

Qy 543 ATTCTTGGAAATTCCTGTCTCTCTGCTCTCTCTGCTCTCTTATTTCAAGTGTACAGATTTACTG 602
Db 418 CACCTCGAGTCTTCACGGCCCTTCTCAGCGTTACCTTCTTCAACCTCAGCATCTACCT 477

Qy 603 GAGCTGTGGAGCG 617
Db 478 GAACATCCAGAGGCG 492
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RESULT 11

CNS03296/c

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LOCUS      CNS03296
DEFINITION Tetraodon nigroviridis genome survey sequence T7 end of clone
            206D09 of library G from Tetraodon nigroviridis, genomic survey
            sequence.
ACCESSION  AL224547.1 GI:7883412
VERSION    AL224547.1
KEYWORDS   GSS; genome survey sequence.
SOURCE     Tetraodon nigroviridis
ORGANISM   Tetraodon nigroviridis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
            Tetraodontoidea; Tetraodontidae; Tetraodon.
REFERENCE  1
AUTHORS    Roest Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
            Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,P.,
            Saurin,W. and Weissenbach,J.
            Estimate of human gene number provided by genome-wide analysis
            using Tetraodon nigroviridis DNA sequence
            Nat. Genet. 25 (2), 235-238 (2000)
PUBMED     20296633
REFERENCE  2
AUTHORS    Roest Crolius,H., Jaillon,O., Dasilva,C., Ozouf-Costaz,C.,
            Fizames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,P.,
            Saurin,W., Bernot,A. and Weissenbach,J.
            Characterization and repeat analysis of the compact genome of the
            freshwater pufferfish Tetraodon nigroviridis
            Genome Res. 10 (7), 939-949 (2000)
PUBMED     20359837
PUBMED     10899143
REFERENCE  3 (bases 1 to 921)
AUTHORS    Direct Submission
            Genoscope.
TITLE      Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seque@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT    This sequence is a single read and was generated as part of a large
            scale clone-end sequencing project of the Tetraodon nigroviridis
            genome. For more information, please take a look at
            http://www.genoscope.cns.fr/tetraodon.
FEATURES   Location/Qualifiers
            source
            1..921
            /organism="Tetraodon nigroviridis"
            /mol_type="genomic DNA"
            /db_xref="taxon:99883"
            /clone="206D09"
            /clone_lib="G"
            /note="Genoscope sequence ID : CONG206CB05LP1-end : T7"

ORIGIN
Query Match      7.6%; Score 89.2; DB 9; Length 921;
Best Local Similarity 59.4%; Pred. No. 6e-15;
Matches 171; Conservative 0; Mismatches 113; Indels 4; Gaps 1;

Qy 889 CTTCTCAGAGCAGGAAGTAGCCAGGTGCGTAGCTGCTCTCTGAGTGCTTTTGCCATT 948
Db 588 CTGTCCAGAGACAAAAGATTGCCAAATCTCTGCCATTATCGCTGTGTTTTCGGGATC 529

Qy 949 TGCTGGGCTCGGTATTCCTGTTTCAAAATGTTCTTTCAACTTATCGCAGGCGGAGCGC 1008
Db 528 TGCTGGGCCCCCTACACGCTGCTGATGATCATCCGCGCGCTGCGAGCGAGTGCCTGG 469

Qy 1009 CCAAAATCGATTTGTACAGCATAGCCTTTTGGCTACAGTGGTTCAATTCACTTATTAAAT 1068
Db 468 CCGACTAC----TGTAGAGATTAACCTTCTGGCTCTGTGGCTCAACTAGCATCAAC 413

Qy 1069 CCCTTTCTATACCTTTGTGCCACAGAGCTTTCCAGAAAGGCTTTCTGGAAGATCTCTGT 1128
Db 412 CCCTTCTGTACCGCTGTGCCACAGCAGCTTCCGAGGGGCTTTCTCCAAGATCCTGTGT 353

Qy 1129 GTGACAAAGCAACCCAGCACCTTTCACAGACCCAGTCAGTATCTTCTTGA 1176
```



Db	352	CCCAAGACAGTCGGTTCAGCCTCAGATCGAAGTCAGTCGTTGTA 305	
RESULT 12			
LOCUS	BQ950659	1046 bp mRNA linear	EST 21-AUG-2002
DEFINITION	AGENCOURT_8863943 NIH_MGC_129 Mus musculus cDNA clone IMAGE:6311932		
5' mRNA sequence.			
ACCESSION	BQ950659		
VERSION	BQ950659.1	GI:22366137	
KEYWORDS	EST.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 1046)		
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/.		
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)		
JOURNAL	Unpublished (1999)		
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapbs-remail.nih.gov Tissue Procurement: Susan L. Sullivan, Ph.D. cDNA Library Preparation: ResGen, Invitrogen Corp cDNA Library Arrayed by: The I.M.A.G.E. Consortium DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM13736 row: k column: 05 High quality sequence stop: 640.		
FEATURES	Location/Qualifiers		
source	1..1046 /organism="Mus musculus" /mol_type="mRNA" /db_xref="taxon:10090" /clone="IMAGE:6311932" /lab_host="DH10B (phage-resistant)" /clone_lib="NIH_MGC_129" /note="Organ: olfactory epithelium; Vector: pCMV-SPORT6.1; Site 1: EcoRV; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 2.2 kb. Constructed by ResGen, Invitrogen Corp. Note: this is a NIH_MGC Library."		
ORIGIN			
Query Match	7.2%	Score 84.2; DB 5; Length 1046;	
Best Local Similarity	56.5%	Pred. No. 2e-13;	
Matches	177; Conservative	0; Mismatches 133; Indels 3; Gaps 1;	
Qy	191	TGGGTGTCATCTCCATTCCTGTGTACATCCCTCACACGCTGTTAAC--TGGAAATTTG 247	
Db	438	TAGTGTGCTTCTGTGATCCCATTTGTATGCTATGCTATGCTGACCGCGGTGGACCTTG 497	
Qy	248	GAAGTGAATCTGATGTTTGGCTCATCTACTACTATCTTTTGTGCACAGCATCCGCTCT 307	
Db	498	GCCGGGCGCTTGAAGCTGTGGTGTGTGTAGTACTACTGTGTGCTCTCTCACTCT 557	
Qy	308	ACAGTATGTCCTCATTTAGTACGATCGATACCAAGTCAGTTTCAAAACGCTGTGCGTTATA 367	
Db	558	TCAACATCGTGTGATCAGCTATACCGGATTCCTGTGTCAGTCACCTCGAGCTGTCTCCCTACC 617	
Qy	368	GAGCACAGCACATGGGATCCTGAAATTTGTGCTCAATGGTGGCTGTTTGGATATCGG 427	
Db	618	GGGCCCCAGAGGGGGACACAGACGGGCTGTTCGGAAGATGGCACTGGTGTGGGTGCTGG 677	
Qy	428	CTTTCTTGGTCAATGGGCCCAATGATTTCTGGCTTCGGATTTCTTGAAGAACAGCACCAACA 487	
Db	678	CTTCTCTGCTATGCGGCTGGCATCTGAGTTGGAGTACCTGTCCGGTGGCACTCCA 737	
Qy	488	CAGAGGAGTGGGA 500	
Db	738	TCCGGAGGGGCCA 750	
RESULT 13			
LOCUS	BC019470		
DEFINITION	Mus musculus cholinergic receptor, muscarinic 2, cardiac, mRNA (cDNA clone IMAGE:4036375), containing frame-shift errors.		
ACCESSION	BC019470		
VERSION	BC019470.1	GI:18044479	
KEYWORDS	HTC.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 1136)		
AUTHORS	Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,P.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Heieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Roehlyuk,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Heiton,E., Kettman,M., Madan,A., Young,A.C., Shevchenko,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Green,E.D., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.		
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences		
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)		
PUBMED	12477932		
REFERENCE	2 (bases 1 to 1136)		
AUTHORS	Strausberg,R.		
TITLE	Direct Submission		
JOURNAL	Submitted (19-DEC-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA		
REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov		
COMMENT	Contact: MGC help desk Email: cgapbs-remail.nih.gov Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center Center code: BCM-HGSC Web site: http://www.hgsc.bcm.tmc.edu/cdna/ Contact: amc@bcm.tmc.edu Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H., Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati, A.N., Gibbs, R.A.		
FEATURES	Location/Qualifiers		
source	1..1136 /organism="Mus musculus" /mol_type="mRNA" /strain="mix FVB/N, C57BL/6J" /db_xref="taxon:10090" /clone="IMAGE:4036375" /tissue_type="Mammary tumor. WAP-TGF alpha model. 7 months		

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov  
Series: IRAC Plate: 37 Row: a Column: 16  
This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not identity to protein  
This clone has the following problem: frame shifted.

old, gross tissue."  
/clone lib="NCI CGAP Mam5"  
/lab host="DH10B"  
/note="Vector: pCMV-SPORT6"

## ORIGIN

Query Match 7.0%; Score 82.2; DB 3; Length 1136;  
Best Local Similarity 56.3%; Pred. No. 8.3e-13;  
Matches 175; Conservative 0; Mismatches 133; Indels 3; Gaps 1;

QY 73 CTTCCTTTTGTATAACGATAGGAATGCTGTGCTGCTTTAGCTTTGTAGCAGACAGA 132  
DB |||||  
QY 133 AACCTTAGACATCGAAGTAATATTTTCTTAATTTGGCTATTTCTGACTTCTTCGTG 192  
DB |||||  
QY 193 GGTGTCATCTCCATTCCTCTGTATCATCTCCTCACAGCGTGTT---AACTGGAATTTTGGG 249  
DB |||||  
QY 688 GGTGTTTTCTCCATGAACCTTGTATACCTCTACACTGTGATTTGGCTACTGGCCCTTTGGGA 747  
DB |||||  
QY 250 AGTGAATCTGCATGTTTTGGCTCATTTACTGACTATCTTTTGTGCACAGCATCGTCTAC 309  
DB |||||  
QY 748 CCTGTAGTGTGCGACCTTTGGCTAGCTTGTGACATGTTGTGCAAAATGCTCCGTTATG 807  
DB |||||  
QY 310 AGTATTCCTCTCAATAGCTAGCATCGATACAGTCAGTTTCAAACGCTGTGCGTTATAGA 369  
DB |||||  
QY 808 AATCTTCTCATCATCAGCTTTGTATAGATCTTCTGTGTCAAAAACCTCTAACCTACCCA 867  
DB |||||

## RESULT 14

BQ837058  
LOCUS  
DEFINITION  
r37e04.y1 Meloidogyne hapla J2 pAMP1 v1 Meloidogyne hapla cDNA 5',  
similar to TR:Q9XW31 Q9XW31 Y40H4A.1 PROTEIN. [1] ; mRNA sequence.  
BQ837058  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Meloidogyne hapla  
Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;  
Tylenchoidea; Heteroderidae; Meloidogyninae; Meloidogyne.  
1 (bases 1 to 505)  
McCart, J., Clifton, S., Chiapelli, B., Pape, D., Martin, J.,  
Wyllie, T., Dante, M., Marra, M., Hillier, L., Kucaba, T., Theising, B.,  
Bowers, Y., Gibbons, M., Ritter, E., Bennett, J., Franklin, C.,  
Taagareishvili, R., Ronko, I., Kennedy, S., Maguire, L., Beck, C.,  
Underwood, K., Steptoe, M., Allen, M., Person, B., Swaller, T.,  
Harvey, N., Schurk, R., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,  
McCann, R., Waterston, R. and Wilson, R.  
The Washington Univ. Nematode EST Project, 1999  
Unpublished (1999)  
Contact: McCarter JP  
The Washington Univ. Nematode EST Project, 1999  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
This clone will not be made available due to an unidentified  
microbial contamination of the source material.  
Seq primer: -40RP from Gibco  
High quality sequence stop: 407.

## FEATURES

source  
1..505  
/organism="Meloidogyne hapla"  
/mol\_type="mRNA"  
/db\_xref="taxon:6305"

/dev\_stage="J2"  
/lab host="DH10B"

/clone lib="Meloidogyne hapla J2 pAMP1 v1"  
/note="Vector: pAMP1 (Gibco); Site 1: NotI; Site 2: SalI;  
The library was constructed by Claire Murphy and Dr. James  
McCart at Washington University, St. Louis. The cDNA was  
made by using Dynabead oligo-dT priming (Dynal). PCR based  
library using a modified protocol from the SMART PCR cDNA  
Synthesis Kit from Clontech. Directionally cloned into the  
UDG sites of pAMP1. J2 were provided by Dr. Valerie  
Williamson of the University of California at Davis  
(vwilliamson@ucdavis.edu)."

## ORIGIN

Query Match 6.8%; Score 79.8; DB 5; Length 505;  
Best Local Similarity 56.0%; Pred. No. 3.3e-12;  
Matches 172; Conservative 0; Mismatches 132; Indels 3; Gaps 1;

QY 77 CTTTGTCTAATACGATAGGCAATGCTGTGCTATTTAGCTTTGTAGCAGACAGAAACC 136  
DB |||||  
QY 45 CATTAGCTACAACGATCGGAATGCTCTTGTATGCTTTCTATTGTGTGATAAAAAT 104  
DB |||||  
QY 137 TTAGACATCGAAGTAATATTTTCTTAATTTGGCTATTTCTGACTTCTTCGTGGGTG 196  
DB |||||  
QY 105 TACAACAATAGCAATATTTTCTTCTCTTAGCTGTGCTGACTTACTATTTGGGC 164  
DB |||||  
QY 197 TCATCTCCATCTCTGTACATCCCTCACAGCGTGTTT---AACTGGAATTTTGGAGTG 253  
DB |||||  
QY 165 TTATTTCTATCTCTTATGTTCTATATACGCAATAGACTTGGACTTTTGGTTATT 224  
DB |||||  
QY 254 GAATCTGCATGTTTTGGCTCATTTACTGACTATCTTTTGTGCACAGCATCCCTTACAGTA 313  
DB |||||  
QY 225 CTCTTTGTCAATCTGCTCTGTATAGATTTAATGTGCAATGCTTTCAGCACTCAATT 284  
DB |||||  
QY 314 TTGTCTCTATTAGCTAGCATCGATACCAAGTCAGTTTCAAACGCTGTGCTTATAGACAC 373  
DB |||||  
QY 285 TGTATTAAATAGCTTTGTATAGATCTTTTCTGTACCCGACCTTAACTTACAGGCCAA 344  
DB |||||

## RESULT 15

BQ836551  
LOCUS  
DEFINITION  
r47e01.y1 Meloidogyne hapla J2 pAMP1 v1 Meloidogyne hapla cDNA 5',  
similar to TR:Q9XW31 Q9XW31 Y40H4A.1 PROTEIN. [1] ; mRNA sequence.  
BQ836551  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Meloidogyne hapla  
Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;  
Tylenchoidea; Heteroderidae; Meloidogyninae; Meloidogyne.  
1 (bases 1 to 410)  
McCart, J., Clifton, S., Chiapelli, B., Pape, D., Martin, J.,  
Wyllie, T., Dante, M., Marra, M., Hillier, L., Kucaba, T., Theising, B.,  
Bowers, Y., Gibbons, M., Ritter, E., Bennett, J., Franklin, C.,  
Taagareishvili, R., Ronko, I., Kennedy, S., Maguire, L., Beck, C.,  
Underwood, K., Steptoe, M., Allen, M., Person, B., Swaller, T.,  
Harvey, N., Schurk, R., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,  
McCann, R., Waterston, R. and Wilson, R.  
The Washington Univ. Nematode EST Project, 1999  
Unpublished (1999)  
Contact: McCarter JP  
The Washington Univ. Nematode EST Project, 1999  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
This clone will not be made available due to an unidentified  
microbial contamination of the source material.  
Seq primer: -40RP from Gibco  
High quality sequence stop: 407.

## TITLE

## JOURNAL

## COMMENT

microbial contamination of the source material.

Seq primer: -4ORP from Gibco.

## FEATURES

source

Location/Qualifiers

1. .410

/organism="Meloiodogone hapla"

/mol\_type="mRNA"

/db\_xref="taxon:6305"

/dev\_stage="J2"

/lab\_host="DH10B"

/clone\_lib="Meloiodogone hapla J2 pAMP1 v1"

/notes="Vector: pAMP1 (Gibco); Site 1: NotI; Site 2: SalI; The library was constructed by Claire Murphy and Dr. James McCarter at Washington University, St. Louis. The cDNA was made by using Dynabead oligo-dT priming (Dyna). PCR based library using a modified protocol from the SMART PCR cDNA Synthesis Kit from Clontech. Directionally cloned into the UDG sites of pAMP1. J2 were provided by Dr. Valerie Williamson of the University of California at Davis (vmwilliamson@ucdavis.edu)."

## ORIGIN

Query Match 6.6%; Score 78.2; DB 5; Length 410;

Best Local Similarity 55.7%; Pred. No. 9.3e-12;

Matches 171; Conservative 0; Mismatches 133; Indels 3; Gaps 1;

Qy	77	CTTTTGTCTAAGCATAGGCAATGCTGTGGTCATTTTAGCCTTTGTAGCAGACAGAAACC	136
Db	45	CATTAGCTACAGATCGGAATGCTCTTGTATGCTTTCTATTTGTGTGATAAAAAAT	104
Qy	137	TTAGACATCGAAGTAATTTATTTTCTTAATTGGCTATTTCTGACTTCTCGTGGGTG	196
Db	105	TACAAACAATTAGCAATTATTTTCTTTCTTTTAGCTGTGCTACTTACTATTGGGC	164
Qy	197	TCATCTCCATTCCTGTGTACATCCCTCACAGCTGTTT---AACTGGAATTTTGGAGTG	253
Db	165	TTATTTCTATTCCTCTTATGACTTTATATACGGCAAAATGAGACTTGGACTTTTGGTTATT	224
Qy	254	GAATCTGCATGTTTGGCTCATTTACTGACTATCTTTTGTGCACAGCATCGTCTACAGTA	313
Db	225	CTCTTTGTCAATTCTGGCTGTGTATAGATTATTATGTGCAATGCTTCAGCACTCAATT	284
Qy	314	TTGTCTCTATTAGTAGCATGATACCAGTCAGTTCAGTTTCAAAACGCTGTGCGTTATAGAGCAC	373
Db	285	TGTTATTAAATTAGTTTGTAGATACCTTTTCTGTACCCGACCTTTAACTTACAGGCCAA	344
Qy	374	AGCACAC	380
Db	345	AGAGAAC	351

Search completed: August 5, 2005, 14:55:23

Job time : 3701 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 3, 2005, 01:34:46 ; Search time 165 Seconds  
(without alignments)  
916.505 Million cell updates/sec

Title: US-10-626-126-9  
Perfect score: 2045  
Sequence: 1 MSENSEGTDLPLTAQVPLAF.....WKILCVTKQAPAPQTSQSVSS 391

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:.\*  
1: geneseqp1980s:.\*  
2: geneseqp1990s:.\*  
3: geneseqp2000s:.\*  
4: geneseqp2001s:.\*  
5: geneseqp2002s:.\*  
6: geneseqp2003as:.\*  
7: geneseqp2003bs:.\*  
8: geneseqp2004s:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2034	99.5	391	5	AAM50566 Rat hist
2	1742	85.2	391	5	AAM50565 Mouse his
3	1742	85.2	391	8	ADO29497 Mouse GPC
4	1403.5	68.6	390	3	AAB02831 Human p
5	1403.5	68.6	390	3	AAV71297 Human orp
6	1403.5	68.6	390	4	AAB62445 Human GPC
7	1403.5	68.6	390	4	AAG64477 Human G p
8	1403.5	68.6	390	4	AAAB73622 Human G p
9	1403.5	68.6	390	5	AAM53050 Human G p
10	1403.5	68.6	390	5	ABP98629 Human his
11	1403.5	68.6	390	5	ABB78276 Amino aci
12	1403.5	68.6	390	5	AAM50564 Human his
13	1403.5	68.6	390	5	AAG66023 Human his
14	1403.5	68.6	390	5	AAU74906 Amino aci
15	1403.5	68.6	390	6	ABU92265 Human G-p
16	1403.5	68.6	390	6	ABU92265 Human G p
17	1403.5	68.6	390	6	ABP81727 Human his
18	1403.5	68.6	390	6	AAE36417 Human H4
19	1403.5	68.6	390	7	ADG98760 Human orp
20	1403.5	68.6	390	7	ADJ26923 Human end
21	1403.5	68.6	390	8	ADG86375 Human his
22	1403.5	68.6	390	8	ADJ88376 Novel hum
23	1403.5	68.6	390	8	ADJ88376 Human his
24	1403.5	68.6	390	8	ADO05720 Human his
25	1403.5	68.6	390	8	ADO29496 Human GPC
26	1403.5	68.6	390	8	ADP20168 Human G p

26	1403.5	68.6	390	8	ADQ75074 Human G p
27	1403.5	68.6	391	5	AAM53052 Human G p
28	1403.5	68.6	392	5	AAM53053 Human G p
29	1398.5	68.4	390	4	AAM51410 Human GPR
30	1398.5	68.4	390	6	AAE36416 Human H4
31	1398.5	68.4	390	8	ADG86522 Human end
32	1237.5	60.5	389	5	AAM50567 Guinea pi
33	1233	60.3	357	6	AAE36415 Human H4
34	1117.5	54.6	336	6	AAE36414 Human H4
35	698	34.1	445	6	ABR43668 Monkey hi
36	698	34.1	445	6	ABP57426 Monkey hi
37	698	34.1	445	8	ADP76111 Monkey H3
38	693	33.9	445	2	AAW92975 Human MAC
39	693	33.9	445	2	AAAY06322 Human G p
40	693	33.9	445	2	AAAG67830 Human mus
41	693	33.9	445	3	AAAY92218 Human his
42	693	33.9	445	4	AAAB30627 A human h
43	693	33.9	445	5	ABB79792 Human his
44	693	33.9	445	6	ABR43667 Human his
45	693	33.9	445	6	ABP57425 Human his

ALIGNMENTS

RESULT 1  
AAM50566  
ID AAM50566 standard; protein; 391 AA.  
XX  
AC AAM50566;  
XX  
DT 18-MAR-2002 (first entry)  
XX  
DE Rat histamine H4 receptor.  
XX  
KW Histamine H4 receptor; rat; antiasthmatic; antiallergenic;  
KW antiinflammatory; cardiac; circulatory; antidiabetic; laxative;  
KW diagnosis; gene therapy.  
XX  
OS Rattus rattus.  
XX  
PN WO200192485-A1.  
XX  
PD 06-DEC-2001.  
XX  
PF 22-FEB-2001; 2001WO-US005914.  
XX  
PR 31-MAY-2000; 2000US-0208260P.  
XX  
PI (ORTH ) ORTHO-MCNEIL PHARM INC.  
XX  
PI Lovenberg T, Liu C;  
XX  
DR WPI; 2002-114339/15.  
XX  
DR N-PSDB; AAI70982.  
XX  
New mammalian histamine H4 receptor proteins and polynucleotides encoding the proteins, useful in gene therapy for treating diseases where it is beneficial to elevate mammalian histamine H4 receptor activity.  
XX  
Claim 13; Fig 6A; 92pp; English.  
XX  
The present sequence is that of a rat histamine receptor of the H4 subtype, as predicted from a cDNA clone isolated from a spleen cDNA library. The invention provides mammalian (human, mouse, rat and guinea pig) histamine H4 receptor nucleic acid molecules (see AAI70980-83) and polypeptides (see AAM50564-67). The nucleic acids have been expressed in recombinant host cells that produce active recombinant protein. The pharmacology of known histamine ligands is demonstrated. Mammalian histamine H4 receptor may be used in gene therapy for the treatment of diseases where it is beneficial to elevate mammalian histamine H4 receptor activity. Recombinant protein is useful for identifying modulators of the histamine H4 receptor. Such modulators may be useful

CC for diagnosing, treating or preventing asthma, allergy, inflammation,  
 CC cardiovascular and cerebrovascular disorders, non-insulin dependent  
 CC diabetes mellitus, hyperglycemia, constipation, arrhythmia, disorders of  
 CC the neuroendocrine system, stress and spasticity  
 XX  
 XX Sequence 391 AA;

Query Match 99.5%; Score 2034; DB 5; Length 391;  
 Best Local Similarity 99.7%; Pred. No. 2.3e-203;  
 Matches 390; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Qy 1 MSESNGTDVLPPLTAQVPLAFMLSLAPAITIGNAVVILAFVADRNLRHRSNYFFLNLAIS 60  
 Db 1 MSESNGTDVLPPLTAQVPLAFMLSLAPAITIGNAVVILAFVADRNLRHRSNYFFLNLAIS 60  
 Qy 61 DFFVGVISIPLYIPHTLFFNNPGSGICMFWLITDYLCTASVYSIVLISYDRYQSVNAV 120  
 Db 61 DFFVGVISIPLYIPHTLFFNNPGSGICMFWLITDYLCTASVYSIVLISYDRYQSVNAV 120  
 Qy 121 RYRAQHTGILKIQAQVAVVILAFVNGPMLASDSWKNSTNTECEPGFVTEWYILAIT 180  
 Db 121 RYRAQHTGILKIQAQVAVVILAFVNGPMLASDSWKNSTNTECEPGFVTEWYILAIT 180  
 Qy 181 AFLEFLLPVSLLVYFVSQIYWSLWKRGLSRCPSHAGFIATSSRGTHSRRTGLACRTSL 240  
 Db 181 AFLEFLLPVSLLVYFVSQIYWSLWKRGLSRCPSHAGFIATSSRGTHSRRTGLACRTSL 240  
 Qy 241 PGLKEPAASLHSESPPRGKSSLLVSLRTHMSGSIIPKVGFCRSESPVLHQREHVELLRG 300  
 Db 241 PGLKEPAASLHSESPPRGKSSLLVSLRTHMSGSIIPKVGFCRSESPVLHQREHVELLRG 300  
 Qy 301 RKLARSIAVLLSAPAIQWAPCYCLFTIVLSTYRGERPKSIWYSIAFWLQFNLSINPFLY 360  
 Db 301 RKLARSIAVLLSAPAIQWAPCYCLFTIVLSTYRGERPKSIWYSIAFWLQFNLSINPFLY 360  
 Qy 361 PLCHRRFQKAPFKILCVTKQAPSPQTSVSS 391  
 Db 361 PLCHRRFQKAPFKILCVTKQAPSPQTSVSS 391

RESULT 2  
 AAM50565  
 ID AAM50565 standard; protein; 391 AA.

XX AAM50565;  
 AC AAM50565;  
 XX 18-MAR-2002 (first entry)  
 XX Mouse histamine H4 receptor.  
 XX Histamine H4 receptor; mouse; antiasthmatic; antiallergenic;  
 KW antiinflammatory; cardiant; circulatory; antidiabetic; laxative;  
 KW diagnosis; gene therapy.

XX Mus musculus.  
 XX WO200192485-A1.  
 XX 06-DEC-2001.  
 XX 22-FEB-2001; 2001WO-US005914.  
 XX 31-MAY-2000; 2000US-0208260P.  
 XX (ORTH ) ORTHO-MCNEIL PHARM INC.

XX Lovenberg T, Liu C;  
 XX WPI; 2002-114339/15.  
 XX N-PSDB; AAI70981.  
 XX New mammalian histamine H4 receptor proteins and polynucleotides encoding  
 the proteins, useful in gene therapy for treating diseases where it is

PT beneficial to elevate mammalian histamine H4 receptor activity.

XX Claim 13; Fig 5B; 92pp; English.

XX The present sequence is that of a mouse histamine receptor of the H4  
 CC subtype, as predicted from a cDNA clone isolated from a spleen cDNA  
 CC library. The invention provides mammalian (human, mouse, rat and guinea  
 CC pig) histamine H4 receptor nucleic acid molecules (see AAI70980-83) and  
 CC polypeptides (see AAM50564-67). The nucleic acids have been expressed in  
 CC recombinant host cells that produce active recombinant protein. The  
 CC pharmacology of known histamine ligands is demonstrated. Mammalian  
 CC histamine H4 receptor may be used in gene therapy for the treatment of  
 CC diseases where it is beneficial to elevate mammalian histamine H4  
 CC receptor activity. Recombinant protein is useful for identifying  
 CC modulators of the histamine H4 receptor. Such modulators may be useful  
 CC for diagnosing, treating or preventing asthma, allergy, inflammation,  
 CC cardiovascular and cerebrovascular disorders, non-insulin dependent  
 CC diabetes mellitus, hyperglycemia, constipation, arrhythmia, disorders of  
 CC the neuroendocrine system, stress and spasticity

XX Sequence 391 AA;

Query Match 85.2%; Score 1742; DB 5; Length 391;

Best Local Similarity 84.9%; Pred. No. 7.5e-173;

Matches 332; Conservative 17; Mismatches 42; Indels 0; Gaps 0;

Qy 1 MSESNGTDVLPPLTAQVPLAFMLSLAPAITIGNAVVILAFVADRNLRHRSNYFFLNLAIS 60  
 Db 1 MSESNGTDVLPPLTAQVPLAFMLSLAPAITIGNAVVILAFVADRNLRHRSNYFFLNLAIS 60  
 Qy 61 DFFVGVISIPLYIPHTLFFNNPGSGICMFWLITDYLCTASVYSIVLISYDRYQSVNAV 120  
 Db 61 DFFVGVISIPLYIPHTLFFNNPGSGICMFWLITDYLCTASVYSIVLISYDRYQSVNAV 120  
 Qy 121 RYRAQHTGILKIQAQVAVVILAFVNGPMLASDSWKNSTNTECEPGFVTEWYILAIT 180  
 Db 121 RYRAQHTGILKIQAQVAVVILAFVNGPMLASDSWKNSTNTECEPGFVTEWYILAIT 180  
 Qy 181 AFLEFLLPVSLLVYFVSQIYWSLWKRGLSRCPSHAGFIATSSRGTHSRRTGLACRTSL 240  
 Db 181 AFLEFLLPVSLLVYFVSQIYWSLWKRGLSRCPSHAGFIATSSRGTHSRRTGLACRTSL 240  
 Qy 241 PGLKEPAASLHSESPPRGKSSLLVSLRTHMSGSIIPKVGFCRSESPVLHQREHVELLRG 300  
 Db 241 PGLKEPAASLHSESPPRGKSSLLVSLRTHMSGSIIPKVGFCRSESPVLHQREHVELLRG 300  
 Qy 301 RKLARSIAVLLSAPAIQWAPCYCLFTIVLSTYRGERPKSIWYSIAFWLQFNLSINPFLY 360  
 Db 301 RKLARSIAVLLSAPAIQWAPCYCLFTIVLSTYRGERPKSIWYSIAFWLQFNLSINPFLY 360  
 Qy 361 PLCHRRFQKAPFKILCVTKQAPSPQTSVSS 391  
 Db 361 PLCHRRFQKAPFKILCVTKQAPSPQTSVSS 391

RESULT 3

ADO29497  
 ID ADO29497 standard; protein; 391 AA.

XX ADO29497;

XX 29-JUL-2004 (first entry)

XX Mouse GPCR HH4, SEQ ID NO:599.

XX G protein-coupled receptor; GPCR; drug screening; diagnosis;  
 KW transgenic mouse; neurological disorder; adrenal gland disorder;  
 KW colon disorder; intestinal disorder; cardiovascular disorder;  
 KW muscular disorder; blood disorder; immune disorder; bone disorder;  
 KW joint disorder; metabolic disorder; nutritive disorder; cancer;  
 KW kidney disorder; liver disorder; lung disorder; breast disorder;  
 KW ovary disorder; uterus disorder; prostate disorder; testis disorder;  
 KW skin disorder; stomach disorder; pancreas disorder; spleen disorder;

KW thymus disorder; thyroid disorder; antiparkinsonian; antimanic;  
KW cystostatic; antiinflammatory; vasotropic; antianginal; antiarrhythmic;  
KW CNS; central nervous system; respiratory; antidiarrhetic; antidiabetic;  
KW virucide; hepatotropic; antibacterial; antianemic; antiseborrheic;  
KW dermatological; antitumor; antithyroid; antiallergic; anorectic;  
KW immunosuppressive; nephrotropic; gene therapy; GPCR modulator; mouse;  
KW murine; receptor.  
XX  
XX Mus musculus.  
XX WO2004040000-A2.  
XX 13-MAY-2004.  
XX  
XX 09-SEP-2003; 2003WO-US028226.  
XX  
XX 09-SEP-2002; 2002US-0409303P.  
XX 09-APR-2003; 2003US-0461329P.  
XX  
XX (PRIM-) PRIMAL INC.  
XX Gaitanaris GA, Bergmann JE, Gragerov A, Hohmann J, Li F;  
XX Madisen L, Mcilwain KL, Pavlova MN, Vassilatis D, Zeng H;  
XX  
XX WPI; 2004-390329/36.  
XX N-PSDB; ADO30257.  
XX  
XX Novel mammalian G protein coupled receptors, useful for identifying  
XX compounds that modulates diagnosing and treating disease condition  
XX associated with GPCR dysfunction e.g. autoimmune diseases, angina  
XX pectoris, Parkinson's disease.

Claim 151; SEQ ID NO 599; 542pp; English.

XX The invention relates to human and mouse G protein-coupled receptors  
XX (GPCRs) and nucleic acids encoding them. The invention also relates to  
XX sequences at least 90% identical to the GPCR proteins and nucleic acids  
XX of the invention; methods of treating, preventing or diagnosing diseases  
XX associated with GPCRs of the invention; methods of screening for  
XX compounds useful in the treatment of GPCR-related diseases; a transgenic  
XX mouse comprising a GPCR gene of the invention; a mouse comprising a  
XX mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived  
XX from the transgenic mice; kits comprising several mice, each of which has  
XX a mutation in a different GPCR gene of the invention; and kits comprising  
XX probes which hybridize to GPCR polynucleotides of the invention. The  
XX invention further discloses variants of the GPCR polypeptides and vectors  
XX comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may  
XX be used in the diagnosis, treatment or prevention of a wide variety of  
XX diseases including neurological disorders (e.g., Alzheimer's disease,  
XX depression, diabetic neuropathy, Parkinson's disease or schizophrenia);  
XX disorders of the adrenal gland; disorders of the colon or intestine  
XX (e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel  
XX syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or  
XX myocardial infarction); muscular disorders; blood disorders (e.g.,  
XX anaemia or leukaemia); immune disorders (e.g., autoimmune disorders or  
XX AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid  
XX arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g.,  
XX obesity, enzyme deficiency-related diseases or vitamin deficiency-related  
XX diseases); and disorders of the kidney, liver, lung, breast, ovary,  
XX uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and  
XX thyroid (e.g., cancers). The present sequence represents a GPCR of the  
XX invention. Note: The full sequence data for this patent did not form part  
XX of the printed specification; those sequences not shown were obtained in  
XX electronic format directly from WIPO at  
XX ftp.wipo.int/pub/published\_pcr\_sequences.

XX Sequence 391 AA;

Query Match 85.2%; Score 1742; DB 8; Length 391;  
Best Local Similarity 84.9%; Pred. No. 7, 5e-173;  
Matches 332; Conservative 17; Mismatches 42; Indels 0; Gaps 0;

OY 1 MSENSTGILPPAAQVPLAFLMSSFAFAIMVGNVILAFVVDRLNLRHSNYFFLNLAIS 60

Db 1 MSENSTGILPPAAQVPLAFLMSSFAFAIMVGNVILAFVVDRLNLRHSNYFFLNLAIS 60  
QY 61 DFFVGVTSIPLYIPIHTLFWNNPGSGICMFWLITDYLLCTASVYSTVLISIDRYQSVSNV 120  
Db 61 DFLVGLISIPLYIPIHTLFWNNPGSGICMFWLITDYLLCTASVYSTVLISIDRYQSVSNV 120  
QY 121 RYRAQHTGILKIVAQMVAWVILAFVNGPMLASDSWKNSTNTBCECPGFVTEWYLAIT 180  
Db 121 SYRAQHTGIMKIVAQMVAWVILAFVNGPMLASDSWKNSTNTKDCPFGFVTEWYLAIT 180  
QY 181 AFLEFLIPVSLVYVSVQIYHSLMKRGSLSRCPHAGSIATSSRCTGHSRRRTGLACRTSL 240  
Db 181 MLEFLIPVSVAVFNVOIYWSLWKRRLSRCPHAGSFSTSSASGHLHAGVACRTSN 240  
QY 241 PGLKEPAASLHSESPRGKSSLLVSLRTHMSGSIITAFKVGSCFCSGSPVLHOREHVELLRG 300  
Db 241 PGLKESAASRHSSESPRKSSILVSLRTHMNSITAFKVGSEFWSSESAALRQREYALLRG 300  
QY 301 RKLARSALVLSAFAICWAPYCLFTIVLSTYRRGERPKSIWYSIAFWLQWNSLNINPLY 360  
Db 301 RKLARSALVLSAFAICWAPYCLFTIVLSTYRRGERPKSVVYSIAFWLQWNSFVNPLY 360  
QY 361 PLCHRRFOKAFWKILCVTKQAPSQTSVSS 391  
Db 361 PLCHRRFOKAFWKILCVTKQAPSQTSVSS 391  
RESULT 4  
AAB02831  
ID AAB02831 standard; protein; 390 AA.  
XX  
XX AAB02831;  
XX  
XX 22-AUG-2000 (first entry)  
XX Human G protein coupled receptor hRUP7 protein SEQ ID NO:14.  
XX Human; G protein coupled receptor; GPCR; transmembrane receptor;  
XX identification; agonist; screening; therapeutic; pharmaceutical; mutant.  
XX Homo sapiens.  
XX WO2000022131-A2.  
XX 20-APR-2000.  
XX  
XX 13-OCT-1999; 99WO-US024065.  
XX  
XX 13-OCT-1998; 98US-00170496.  
XX 12-NOV-1998; 98US-0108029P.  
XX 20-NOV-1998; 98US-0109213P.  
XX 27-NOV-1998; 98US-0110060P.  
XX 16-FEB-1999; 99US-0120416P.  
XX 26-FEB-1999; 99US-0121852P.  
XX 12-MAR-1999; 99US-0123944P.  
XX 12-MAR-1999; 99US-0123945P.  
XX 12-MAR-1999; 99US-0123946P.  
XX 12-MAR-1999; 99US-0123948P.  
XX 12-MAR-1999; 99US-0123949P.  
XX 12-MAR-1999; 99US-0123951P.  
XX 28-MAY-1999; 99US-0136436P.  
XX 28-MAY-1999; 99US-0136437P.  
XX 28-MAY-1999; 99US-0136439P.  
XX 28-MAY-1999; 99US-0137127P.  
XX 28-MAY-1999; 99US-0137131P.  
XX 28-MAY-1999; 99US-0137567P.  
XX 29-JUN-1999; 99US-0141448P.  
XX 27-AUG-1999; 99US-0151114P.  
XX 03-SEP-1999; 99US-0152524P.  
XX 29-SEP-1999; 99US-0156555P.  
XX 29-SEP-1999; 99US-0156633P.  
XX 29-SEP-1999; 99US-0156634P.

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PR 29-SEP-1999; 99US-0156653P.
PR 01-OCT-1999; 99US-0157280P.
PR 01-OCT-1999; 99US-0157281P.
PR 01-OCT-1999; 99US-0157282P.
PR 01-OCT-1999; 99US-0157293P.
PR 01-OCT-1999; 99US-0157294P.
PR 12-OCT-1999; 99US-00416760.
PR 12-OCT-1999; 99US-00417044.
XX (AREN-) ARENA PHARM INC.
PA Behan DP, Lehmann-Bruinsma K, Chalmers DT, Chen R, Dang HT,
PI Gore M, Liaw CW, Lin I, Lowitz K, White C;
XX WPI; 2000-317986/27.
DR N-PSDB; AAA46023.
XX Non-endogenous, human G protein-coupled receptors for screening receptor,
PT inverse or partial agonists useful as therapeutic agents.
XX Example 1; Page 89-90; 187pp; English.
XX The present invention describes transmembrane receptors, preferably human
CC G protein coupled receptors (GPCR), for which the endogenous ligand is
CC unknown (orphan GPCR receptors). More specifically the present invention
CC relates to non-endogenous, constitutively activated versions of a human
CC GPCR. These non-endogenous human GPCRs can be useful for the direct
CC identification of candidate compounds as receptors agonists, inverse
CC agonists or partial agonists for use as pharmaceutical agents. AAA46017
CC to AAA46126 and AAB02825 to AAB02859 represent sequences used in the
CC exemplification of the present invention
XX Sequence 390 AA;
QY Query Match 68.6%; Score 1403.5; DB 3; Length 390;
Best Local Similarity 69.1%; Pred. No. 1.7e-137;
Matches 271; Conservative 40; Mismatches 78; Indels 3; Gaps 2;
QY 1 MSESNGTDVLP LTAQVPLAFMLSLAFATIGNAVILAFVADNLRHRSNYFFLNLAIS 60
DB 1 MPDTNSTINLSLSTRTVTLAFMSSLVAFALMGNALVILAFVVDKNLRHRSYFFLNLAIS 60
QY 61 DFFVGVISIPILYIPHTLFNNWPGSGICMFWLITDYLCTASVYISIVLSYDRYQSVSNV 120
DB 61 DFFVGVISIPILYIPHTLFEWDFGKEICVFWLITDYLCTASVYINVLISYDRYLSVSNV 120
QY 121 RYRAQHTGILKIVAQVAVMTLAFVNGPMILASDSWKNSTNTECBPGFVTEWYILAIT 180
DB 121 SYRQHTGVLTIVLMAVAVYLAFLVNGPMILVSESNKDEGS--ECBPFPFSEWYILAIT 178
QY 181 AFLEFLLPVSLVYVPSVQIYWSLWKGRSLSRCPSHAGFIATSSRGTHSRRTGLACTSL 240
DB 179 SFLEFVLPVILVAYFNMYWSLWKDRHLSRCQSHGLTAVSSNICGHSFGRLLSRSL 238
QY 241 PGLKEPAASLHSPRGKSSLLVSLRTHMSGIITAFKVGSCFSESPVLHOREHVELLRG 300
DB 239 SASTEVPASPHSEQRKSSLMFSRTKMSNTTASRWGFSQSDSVALHOREHVELLRA 298
QY 301 RKLARSVALVLSAFAICWAPYCLFTIVLSYRRGERPKSIWYSIAFLQWNSLINPPLY 360
DB 299 RRLAKSLAILLGVFAVCWAPYSLFTIVLSYSSATGPKSVMYRIAFWLFQWNSPVNPLY 358
QY 361 PLCHRRQKAPWKILCVTKQAPSQ--TQSUS 391
DB 359 PLCHRRQKAPKILFCIKKQPLPSQHSRSVSS 390
RESULT 5
AY71297
ID AA71297 standard; protein; 390 AA.
XX AC AY71297;
XX
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02-NOV-2000 (first entry)

Human orphan G protein-coupled receptor hrUP7.

Human; orphan G protein-coupled receptor; GPCR; hrUP7; drug screening;

transmembrane receptor; signal cascade.

Homo sapiens.

WO200031258-A2.

02-JUN-2000.

13-OCT-1999; 99WO-US023687.

20-NOV-1998; 98US-0109213P.

16-FEB-1999; 99US-0120416P.

26-FEB-1999; 99US-0121852P.

12-MAR-1999; 99US-0123946P.

12-MAR-1999; 99US-0123949P.

28-MAY-1999; 99US-0136436P.

28-MAY-1999; 99US-0136437P.

28-MAY-1999; 99US-0136439P.

28-MAY-1999; 99US-0136567P.

28-MAY-1999; 99US-0137127P.

28-MAY-1999; 99US-0137131P.

29-JUN-1999; 99US-0141448P.

29-SEP-1999; 99US-0156555P.

29-SEP-1999; 99US-0156633P.

29-SEP-1999; 99US-0156634P.

29-SEP-1999; 99US-0156653P.

01-OCT-1999; 99US-0157280P.

01-OCT-1999; 99US-0157281P.

01-OCT-1999; 99US-0157282P.

01-OCT-1999; 99US-0157293P.

01-OCT-1999; 99US-0157294P.

12-OCT-1999; 99US-00416760.

12-OCT-1999; 99US-00417044.

(AREN-) ARENA PHARM INC.

Chen R, Dang HT, Liaw CW, Lin I;

WPI; 2000-400068/34.

N-PSDB; AAD01124.

Novel human orphan G protein-coupled receptors and the encoding cDNAs for use in the identification of G protein-coupled receptor agonists.

Claim 26; Page 60-61; 102pp; English.

The present amino acid sequence is the hrUP7, an endogenous human orphan G protein-coupled receptor (GPCR). The full length hrUP7 cDNA was cloned by RT-PCR using human peripheral leucocyte cDNA as template. The orphan GPCR of the invention, like all GPCRs has seven transmembrane alpha helices with an extracellular N-terminus and an intracellular C-terminus. However, no endogenous ligands has yet been identified for the proteins of the invention. The orphan GPCRs may be used in the identification of their endogenous ligands, and to screen potential GPCR agonists and antagonists for use as pharmaceutical agents. The proteins may also be used in the study of GPCR-mediated signalling cascades, and to elucidate their precise role in normal and diseased human conditions. Nucleic acid encoding human orphan GPCRs may be used for tissue localisation in expression analysis to provide information about their function in healthy and pathological states

Sequence 390 AA;

Query Match 68.6%; Score 1403.5; DB 3; Length 390;

Best Local Similarity 69.1%; Pred. No. 1.7e-137;

Matches 271; Conservative 40; Mismatches 78; Indels 3; Gaps 2;

QY 1 MSESNGTDVLP LTAQVPLAFMLSLAFATIGNAVILAFVADNLRHRSNYFFLNLAIS 60

DB 1 MPDTNSTINLSLSTRTVTLAFMSSLVAFALMGNALVILAFVVDKNLRHRSYFFLNLAIS 60

QY 61 DFFVGVISIPILYIPHTLFNNWPGSGICMFWLITDYLCTASVYISIVLSYDRYQSVSNV 120

DB 61 DFFVGVISIPILYIPHTLFEWDFGKEICVFWLITDYLCTASVYINVLISYDRYLSVSNV 120

QY 121 RYRAQHTGILKIVAQVAVMTLAFVNGPMILASDSWKNSTNTECBPGFVTEWYILAIT 180

DB 121 SYRQHTGVLTIVLMAVAVYLAFLVNGPMILVSESNKDEGS--ECBPFPFSEWYILAIT 178

QY 181 AFLEFLLPVSLVYVPSVQIYWSLWKGRSLSRCPSHAGFIATSSRGTHSRRTGLACTSL 240

DB 179 SFLEFVLPVILVAYFNMYWSLWKDRHLSRCQSHGLTAVSSNICGHSFGRLLSRSL 238

QY 241 PGLKEPAASLHSPRGKSSLLVSLRTHMSGIITAFKVGSCFSESPVLHOREHVELLRG 300

DB 239 SASTEVPASPHSEQRKSSLMFSRTKMSNTTASRWGFSQSDSVALHOREHVELLRA 298

QY 301 RKLARSVALVLSAFAICWAPYCLFTIVLSYRRGERPKSIWYSIAFLQWNSLINPPLY 360

DB 299 RRLAKSLAILLGVFAVCWAPYSLFTIVLSYSSATGPKSVMYRIAFWLFQWNSPVNPLY 358

QY 361 PLCHRRQKAPWKILCVTKQAPSQ--TQSUS 391

DB 359 PLCHRRQKAPKILFCIKKQPLPSQHSRSVSS 390

RESULT 5

AY71297

ID AA71297 standard; protein; 390 AA.

XX AC AY71297;

XX



```
Db 1 MPDNTNLSLSTRVTLAFAFMSLVAFAMLGNALVILAFVVDKRLHRSYFFFLNLALS 60
Qy 61 DFFVGVISIPILYIPHTLFNNMPPGSGICMFWLITDYLCTASVYSIVLISYDRYOSVNAV 120
Db 61 DFFVGVISIPILYIPHTLFNNMPPGSGICMFWLITDYLCTASVYSIVLISYDRYOSVNAV 120
Qy 121 RYRAQHTGILKIVAQMAVWILAFVNGPMLASDSWKNSTNTECEPGFVTEWYILAIT 180
Db 121 SYRTQHTGVLKIVLMAVWVLAFLVNGPMLASDSWKNSTNTECEPGFVTEWYILAIT 178
Qy 181 AFLEFLPLVSLVAVVFSVQIYWSLWKGSLRCPHAGFIATSSRGTHSRRTGLACRTSL 240
Db 179 SFLEFVPIVLVAFYNNIYWSLWKRDLHSCQHPGLTAVSSNICHSFGRLSRRSL 238
Qy 241 PGLKEPAASLHSESPRGKSLLSVLRTHMGSIIAFKVGSCRSSESPVLHQHREHVELLRG 300
Db 239 SASTEVPAFHSERQRKSSLMFSSRTKMSNTTASKMGFSQSDSVLHQHREHVELLRA 298
Qy 301 RKLARSUAVLSAFAICWAPYCLFTIVLSTYRRGERPKSIWYSTAFWLOWNSLINPLY 360
Db 299 RRLAKSLAILLGVFAVCWAPYSLFTIVLSFYSSATGPKSVWYRIAFWLOWNSFVNPPLY 358
Qy 361 PLCHRRFQKAFWKILCVTKQAPSQ-TOSVSS 391
Db 359 PLCHRRFQKAFWKILCVTKQAPSQ-TOSVSS 390

RESULT 6
AAB62445
ID AAB62445 standard; protein; 390 AA.
XX AC AAB62445;
XX DT 09-JUL-2001 (first entry)
XX DE Human GPCR-like polypeptide, PFI-013.
XX KW G-protein coupled receptor; GPCR; PFI-013; antiallergic; antiasthmatic;
XX KW antiinflammatory; vasotropic; antidiabetic; anorectic; cytostatic; human;
XX KW osteopathic; neuroprotective; nootropic; dermatological; gynecological;
XX KW signal transduction.
XX OS Homo sapiens.
XX PN EP1096009-A1.
XX PD 02-MAY-2001.
XX PF 24-OCT-2000; 2000EP-00309364.
XX PR 29-OCT-1999; 99GB-00025641.
XX PR 20-APR-2000; 2000GB-00009973.
XX XX (PFIZ ) PFIZER LTD.
XX FA (PFIZ ) PFIZER INC.
XX XX Peter B, O'reilly MA;
XX PI WPI; 2001-309854/33.
XX DR N-PSDB; AAF83203.
XX XX New G-protein coupled receptor-like polypeptide, polynucleotide for
XX PT screening drug candidates for treating diseases associated with signal
XX PT transduction e.g. allergic, inflammatory, pulmonary, neoplastic diseases.
XX XX Claim 22; Page 44; 66pp; English.
XX XX This is a human G-protein coupled receptor (GPCR)-like polypeptide, PFI-
XX CC 013, encoded by cDNA of NCTMB 41073. The PFI-013 protein can be expressed
XX CC by standard recombinant methodology. Antibodies and modulators of PFI-013
XX CC are useful in the manufacture of a medicament for treating allergic
XX CC disorder, including extrinsic asthma, immunological disorders, such as
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CC intrinsic asthma, vasculitic granulomatous disease, interstitial and
CC other pulmonary disease, including chronic obstructive pulmonary disease
CC (COPD), infectious, inflammatory disease, such as inflammatory bowel
CC disease and neoplastic and myeloproliferative diseases. They are also
CC useful for treating obesity, diabetes, metabolic, neurological diseases,
CC psychotherapeutics, urogenital disease, reproduction and sexual medicine,
CC inflammation, cancer, tissue repair, dermatology, photogeing, skin
CC pigmentation, osteoporosis, cardiovascular, gastrointestinal diseases,
CC allergy and respiratory disease, sensory organ disorders, sleep disorders
CC and hair loss. The PFI-013 protein and nucleic acid are useful in the
CC diagnosis and treatment of the above conditions and also for screening
CC drug candidates for the treatment of diseases associated with signal
CC transduction. The antibodies are also useful for enrichment of
CC eosinophils from mammalian, especially human blood and for detecting the
CC protein in biological samples
XX SQ Sequence 390 AA;
XX
Query Match 68.6%; Score 1403.5; DB 4; Length 390;
Best Local Similarity 69.1%; Pred. No. 1.7e-137;
Matches 271; Conservative 40; Mismatches 78; Indels 3; Gaps 2;
Qy 1 MSESNGTDVLPVLAQVPLAFVLAFAITIGNAVWILAFVADRNLRHRSYFFFLNLALS 60
Db 1 MPDNTNLSLSTRVTLAFAFMSLVAFAMLGNALVILAFVVDKRLHRSYFFFLNLALS 60
Qy 61 DFFVGVISIPILYIPHTLFNNMPPGSGICMFWLITDYLCTASVYSIVLISYDRYOSVNAV 120
Db 61 DFFVGVISIPILYIPHTLFNNMPPGSGICMFWLITDYLCTASVYSIVLISYDRYOSVNAV 120
Qy 121 RYRAQHTGILKIVAQMAVWILAFVNGPMLASDSWKNSTNTECEPGFVTEWYILAIT 180
Db 121 SYRTQHTGVLKIVLMAVWVLAFLVNGPMLASDSWKNSTNTECEPGFVTEWYILAIT 178
Qy 181 AFLEFLPLVSLVAVVFSVQIYWSLWKGSLRCPHAGFIATSSRGTHSRRTGLACRTSL 240
Db 179 SFLEFVPIVLVAFYNNIYWSLWKRDLHSCQHPGLTAVSSNICHSFGRLSRRSL 238
Qy 241 PGLKEPAASLHSESPRGKSLLSVLRTHMGSIIAFKVGSCRSSESPVLHQHREHVELLRG 300
Db 239 SASTEVPAFHSERQRKSSLMFSSRTKMSNTTASKMGFSQSDSVLHQHREHVELLRA 298
Qy 301 RKLARSUAVLSAFAICWAPYCLFTIVLSTYRRGERPKSIWYSTAFWLOWNSLINPLY 360
Db 299 RRLAKSLAILLGVFAVCWAPYSLFTIVLSFYSSATGPKSVWYRIAFWLOWNSFVNPPLY 358
Qy 361 PLCHRRFQKAFWKILCVTKQAPSQ-TOSVSS 391
Db 359 PLCHRRFQKAFWKILCVTKQAPSQ-TOSVSS 390

RESULT 7
AAG64477
ID AAG64477 standard; protein; 390 AA.
XX AC AAG64477;
XX XX 25-SEP-2001 (first entry)
XX DT Human G protein-coupled receptor protein BG26.
XX DE Human; G protein-coupled receptor protein BG26; histamine H3; histamine;
XX KW altering intracellular CAMP concentration;
XX KW regulating signal transduction.
XX OS Homo sapiens.
XX PN WO200146414-A1.
XX XX 28-JUN-2001.
XX PF 20-DEC-2000; 2000WO-JP009038.
XX XX
```

PR 20-DEC-1999; 99JP-00361687.  
XX (BANY ) BANYU PHARM CO LTD.  
XX Itadani H, Nakamura T, Tanaka K, Ohta M;  
XX WPI; 2001-441675/47.  
DR N-PSDB; AAH47911.  
XX  
PT G protein-coupled receptor protein BG26, with activity of binding to  
PT histamine and capable of changing intracellular cAMP concentration in  
PT response to its stimulus, applicable as tool in screening ligands or drug  
PT candidates.  
XX  
XX  
XX Claim 1; Page 41-44; 50pp; Japanese.  
XX  
XX The present sequence is that of the human G protein-coupled receptor  
CC protein BG26, which shows significant homology with histamine H3, with  
CC activity of binding to histamine and capable of changing intracellular  
CC cAMP concentration in response to its stimulus. The protein is applicable  
CC as a tool in screening ligands or drug candidates for regulating signal  
CC transduction from such protein and treating diseases associated with its  
CC abnormality  
XX  
SQ Sequence 390 AA;  
Query Match 68.68; Score 1403.5; DB 4; Length 390;  
Best Local Similarity 69.18; Pred. No. 1.7e-137;  
Matches 271; Conservative 40; Mismatches 78; Indels 3; Gaps 2;  
QY 1 MSBSGGDVLPLTAQVPLAFMLSLAFATIGNAVVILAFVADNRNLRHGRNYPFLNLAIS 60  
DB 1 MPTNSTINLSLSTRVTLAFMSLVAFMILGNALVILAFVDKVLRRSSYFPLNLAIS 60  
QY 61 DFFVGVISIPLYIPHTLFFNPNPGSGICMFWLITDYLCTASVYSIVLISYDRYQSVNAV 120  
DB 61 DFFVGVISIPLYIPHTLFFNPNPGSGICMFWLITDYLCTASVYNVILISYDRYQSVNAV 120  
QY 121 RYRAQHTGILKIYQAVVAVILAFVNGPMLASDSWNKSTNTECEPGFVTEHYILAIT 180  
DB 121 SYRTQHTGVILKIVTLMAVAVLAFVNGPMLVLSSEWKBDEGS--ECPGPFSEHYILAIT 178  
QY 181 AFLEFLPLSVLVVYFVQIYVMSLWKRGLRCPSHAGFIATSSRGTHSRRTGLACRTSL 240  
DB 179 SPLEFVPLVILVAFVNNITVSLWKRDLRCQHPGLTAVSSNICHSFAGRLSSRRSL 238  
QY 241 PGLKEPAASLHSESPROKSSLLVSLRTHMSGSIITAPKVGFRCRSESPVLHQREHVELRG 300  
DB 239 SASTEVPAFSPHERQRKSSLMFSSRTKMSNTIASKMGSPSQSDSVALHQREHVELRA 298  
QY 301 RKLARSLAVLLSAPAIQWAPCYCLETVLSTYRGERPKSIWYSTAFWLQWNSLINPFLY 360  
DB 299 RRLAKSAILLGVFAVCWAPYSLFTIVLSFYSSATGPKSVMYRTAFWLQWNSFVNPFLY 358  
QY 361 PLCHRRFQKAFWKILCVTKOPAPSQ--TOSVSS 391  
DB 359 PLCHRRFQKAFWKILCVTKOPAPSQ--TOSVSS 390  
RESULT 8  
AAB73622  
ID AAB73622 standard; protein; 390 AA.  
AC AAB73622;  
XX  
XX 10-AUG-2001 (first entry)  
XX  
XX Human G protein-coupled receptor AXOR35.  
XX AXOR35; human; G protein-coupled receptor; 7TM receptor;  
KW histamine H3 receptor homologue; infection; viral; bacterial; fungal;  
KW protozoan; HIV-1; HIV-2; pain; cancer; diabetes; obesity; anorexia;  
KW bulimia; osteoporosis; asthma; allergy; urinary retention;

KW acute heart failure; hypotension; hypertension; angina pectoris;  
KW myocardial infarction; stroke; ulcer; migraine; vomiting;  
KW psychotic disorder; neurological disorder; anxiety; schizophrenia;  
KW manic depression; bipolar disorder; depression; delirium; dementia;  
KW severe mental retardation; dyskinesia; Parkinson's disease;  
KW Huntington's disease; Gilles de la Tourette's syndrome; lymphocyte;  
KW macrophage; eosinophil; neutrophil; function modulation;  
KW autoimmune disorder; pulmonary disorder; gene therapy; vaccine;  
KW drug screening; signal transduction; transgenic animal; drug discovery.  
XX Homo sapiens.  
OS  
PN WO200133221-A1.  
XX  
XX 10-MAY-2001.  
XX  
XX 26-OCT-2000; 2000MO-US029461.  
XX  
XX 02-NOV-1999; 99US-00431898.  
PR 03-FEB-2000; 2000US-00497790.  
XX  
XX (SMIK ) SMITHKLINE BEECHAM PLC.  
PA (SMIK ) SMITHKLINE BEECHAM PLC.  
XX  
XX Aubart KM, Bergsma DJ, Fitzgerald LR, Graybill TL, Li X;  
PI Michalovich D, Morrow DM, Zhu Y;  
XX  
DR WPI; 2001-316464/33.  
DR N-PSDB; AAH24007.  
XX  
PT Novel G-protein coupled receptor polypeptide and polynucleotide for  
PT treating cancer, autoimmune, pulmonary, cardiovascular and neurological  
PT disorders and for identifying modulators useful for treating asthma.  
XX  
XX Claim 1; Page 50-51; 54pp; English.  
XX  
XX The invention relates to the human G protein-coupled receptor AXOR35  
CC (AAB73621), to cDNA encoding AXOR35 (AAH24006), and to AXOR35 fragments  
CC and variants. Like all G protein-coupled receptors, AXOR35 has 7 putative  
CC transmembrane domains and is involved in signal transduction. AXOR35 has  
CC homology and structural similarity with G protein-coupled receptors such  
CC as the human histamine H3 receptor. The invention also relates to  
CC expression vectors and host cells comprising AXOR35 DNA, to recombinant  
CC expression of AXOR35, and to an AXOR35-specific antibody. AXOR35 proteins  
CC and nucleotides may be used to treat a wide variety of disorders  
CC including bacterial, fungal, protozoal and viral infections, particularly  
CC HIV-1 or HIV-2 infections; pain; cancer; benign prostatic hypertrophy;  
CC diabetes; obesity; anorexia; bulimia; osteoporosis; asthma; allergies;  
CC urinary retention; acute heart failure; hypotension; hypertension; angina  
CC pectoris; myocardial infarction; stroke; ulcers; migraine; vomiting;  
CC psychotic and neurological disorders such as anxiety, schizophrenia,  
CC manic depression, depression, delirium, dementia, and severe mental  
CC retardation, and dyskinesias, such as Parkinson's disease, Huntington's  
CC disease or Gilles de la Tourette's syndrome. AXOR35 proteins and  
CC nucleotides are useful as vaccines, and AXOR35 proteins, nucleotides and  
CC antibodies may be used in screening compounds for their ability to  
CC modulate AXOR35 activity or expression. Such AXOR35 modulators are  
CC particularly useful for treating asthma, and inhibiting or promoting the  
CC function of lymphocytes, macrophages, eosinophils or neutrophils in  
CC asthmatic lung. AXOR35 proteins, nucleotides and antibodies are also  
CC useful for diagnosing or determining susceptibility of an individual to a  
CC disease via the detection of abnormal levels of protein or mRNA, or via  
CC the detection of mutations in the corresponding gene. AXOR35 proteins are  
CC also useful for inducing an immunological response in a mammal against  
CC the above diseases, and for antibody production. AXOR35 nucleotides are  
CC also useful as diagnostic reagents, in chromosome localisation and tissue  
CC expression studies, and for producing transgenic animals useful in drug  
CC discovery. AXOR35-specific antibodies are useful for purifying the AXOR35  
CC protein or fragments thereof, and are also useful for treating conditions  
CC associated with the expression of the AXOR35 protein. The present  
CC sequence represents human AXOR35  
XX  
XX Sequence 390 AA;

Db 121 SYRQHTGVLIKIVTLMAVAVMLAFVLNPGMILVSESWKDEGS--ECEPGFFSEWYILAIT 178  
 QY 181 AFLEFLLPVSLVYFVVOIYWSLWKRGLRCPHAGFIATSSRGTHGSRRTGLACRTSL 240  
 Db 179 SFLEFVLPVLVAYFNNIYWSLWKRDLHRCQSHPGLTAVSSNICGSPRGLSSRRSL 238  
 QY 241 PGLKEPAASLHSESPRGKSLVSLRTHMGSIIFKVGFCRSESPVLHQREHVELLRG 300  
 Db 239 SASTEVPAFSPHSESRQRKSLMFSSRTKMSNTIASKMGFSQSDSVALHQREHVELLRA 298  
 QY 301 RKLARSIAVLLSAFAICWAPYCLFTIVLSTYRGERPKSIWYSIAFWLQFNLSINPPLY 360  
 Db 299 RRLAKSLAILLGVFAVCWAPYSLFTIVLSFYSSATGPKSVYRIAFWLQFNSEFNPPLY 358  
 QY 361 PLCHRRFQKAFWKILCVTKOPAPSQ-TQSVSS 391  
 Db 359 PLCHKRFQKAFWKILCVTKOPAPSQ-TQSVSS 390

RESULT 10  
 ABP98629  
 ID ABP98629 standard; protein; 390 AA.  
 XX AC ABP98629;  
 XX DT 13-JUN-2003 (first entry)  
 XX DE Human histamine receptor SP9144.  
 XX KW human; histamine receptor; chromosome 18; anti-inflammatory;  
 KW anti-asthmatic; anti-allergic; dermatological; cerebroprotective; stroke;  
 KW anti-migraine; anti-rheumatic; anti-arthritis; antipsoriatic;  
 KW neuroprotective; inflammation; asthma; allergy; atopic dermatitis;  
 KW myocardial infarction; migraine; chronic obstructive pulmonary disease;  
 KW rheumatoid arthritis; multiple sclerosis; inflammatory bowel disease;  
 KW psoriasis; receptor.  
 XX OS Homo sapiens.  
 XX PN US6204017-B1.  
 XX PD 20-MAR-2001.  
 XX PF 07-OCT-1999; 99US-00414010.  
 XX PR 07-OCT-1999; 99US-00414010.  
 XX PS (SCHE ) SCHERING CORP.  
 XX PI Behan JX, Hedrick JA, Laz TM, Monsma FJ, Morsee KL, Umland SP;  
 XX PI Wang S;  
 XX DR WPI; 2002-442063/47.  
 XX DR N-PSDB; ABZ80663.

XX New nucleic acid encoding antigenic part of human histamine receptor,  
 PT useful for preparing antibodies, e.g. for treating-histamine related  
 PT disorders.

XX Example 1; Col 27-30; 19pp; English.

XX This sequence represents the amino acid sequence of a human histamine  
 CC receptor (HR) designated SP9144. The sequence was isolated by searching  
 CC databases with the sequence of known G-coupled protein receptor (GPCR).  
 CC The gene is used for recombinant production of HR and for preparing  
 CC antibodies (Ab). These Ab are used to purify HR by immunoaffinity  
 CC chromatography, in immunoassay of histamine receptor, to identify cDNA  
 CC clones that express the receptor, as antagonist to block binding of  
 CC histamine (for treating any histamine-associated disorder) and to  
 CC generate anti-idiotypic antibodies. Agonists and antagonists of the HR  
 CC protein can be used in the treatment of e.g. inflammation, asthma,  
 CC allergy, atopic dermatitis, stroke, myocardial infarction, migraine,  
 CC chronic obstructive pulmonary disease, rheumatoid arthritis, multiple

CC sclerosis, inflammatory bowel disease and psoriasis

XX SQ Sequence 390 AA;

Query Match 68.6%; Score 1403.5; DB 5; Length 390;  
 Best Local Similarity 69.1%; Pred. No. 1.7e-137;  
 Matches 271; Conservative 40; Mismatches 78; Indels 3; Gaps 2;

QY 1 MSESNGTDVLPALTAQVPLAFMLSLAFAITIGNAVILAFVADRNLRHRSYFFLNLAIS 60

Db 1 MPDTNSTINLSLSTRVTLAFMNSLVAFIMLGNALVILAFVADRNLRHRSYFFLNLAIS 60

QY 61 DFFVGVISIPLYIPHTLFFNNPGSGICMFWLITDYLCTASVISIVLISYDRYQSVNAV 120

Db 61 DFFVGVISIPLYIPHTLFFNMDFGKEICVFWLITDYLCTASVINVLISYDRYLSVNAV 120

QY 121 RYRAQHTGILKIQAQVAVVILAFVLNPGMILASDSKNSNTNTECEPGFVTEWYILAIT 180

Db 121 SYRQHTGVLIKIVTLMAVAVMLAFVLNPGMILVSESWKDEGS--ECEPGFFSEWYILAIT 178

QY 181 AFLEFLLPVSLVYFVVOIYWSLWKRGLRCPHAGFIATSSRGTHGSRRTGLACRTSL 240

Db 179 SFLEFVLPVLVAYFNNIYWSLWKRDLHRCQSHPGLTAVSSNICGSPRGLSSRRSL 238

QY 241 PGLKEPAASLHSESPRGKSLVSLRTHMGSIIFKVGFCRSESPVLHQREHVELLRG 300

Db 239 SASTEVPAFSPHSESRQRKSLMFSSRTKMSNTIASKMGFSQSDSVALHQREHVELLRA 298

QY 301 RKLARSIAVLLSAFAICWAPYCLFTIVLSTYRGERPKSIWYSIAFWLQFNLSINPPLY 360

Db 299 RRLAKSLAILLGVFAVCWAPYSLFTIVLSFYSSATGPKSVYRIAFWLQFNSEFNPPLY 358

QY 361 PLCHRRFQKAFWKILCVTKOPAPSQ-TQSVSS 391

Db 359 PLCHKRFQKAFWKILCVTKOPAPSQ-TQSVSS 390

RESULT 11

ABB78276

ID ABB78276 standard; protein; 390 AA.

XX AC ABB78276;

XX DT 05-DEC-2002 (first entry)

XX DE Amino acid sequence of human histamine receptor.

XX KW Human; histamine receptor; receptor; inflammation; asthma; allergy;  
 KW atopic dermatitis; stroke; myocardial infarction; migraine;  
 KW chronic obstructive pulmonary disease; COPD; rheumatoid arthritis;  
 KW multiple sclerosis; inflammatory bowel disease; psoriasis;  
 KW intracellular second messenger pathway; cellular growth rate;  
 KW hormone secretion.

XX OS Homo sapiens.

XX PN US2002098539-A1.

XX PD 25-JUL-2002.

XX PF 19-MAR-2001; 2001US-00812216.

XX PR 07-OCT-1999; 99US-00414010.

XX PA (BEHA/) BEHAN J X.

XX PA (HEDR/) HEDRICK J A.

XX PA (LAZT/) LAZ T M.

XX PA (MONS/) MONSMA F J.

XX PA (MORS/) MORSE K L.

XX PA (UMLA/) UMLAND S P.

XX PA (WANG/) WANG S.

XX PI Behan JX, Hedrick JA, Laz TM, Monsma FJ, Morsee KL, Umland SP;

Query Match		68.6%;	Score 1403.5;	DB 4;	Length 390;
Best Local Similarity		69.1%;	Pred. No. 1.7e-137;		
Matches		271;	Conservative	40;	Mismatches 78; Indels 3; Gaps 2;
Qy	1	MSENGTDLVPLTAQVPLAFMLSLAFITGNNAVILAFVADNRNLRHSYFFFLNLAIS	60		
Db	1	MPDNTSTINLSLSTRVTLAPFMSLVAFALMGNALVILAFVVDKNLRHSYFFFLNLAIS	60		
Qy	61	DFPVGVISIPLYIPHTLFPNNPGSGICMFWLITDYLLCTASVYSIVLSIDRYQSVNAV	120		
Db	61	DFPVGVISIPLYIPHTLFEWDFGKEICVFWLITDYLLCTASVYINVLISIDRYLSVNAV	120		
Qy	121	RYRAQHTGILKIVAQMAVWILAFVLNPGMILADSGNKNSTNTECEPGFVTEWYILAIT	180		
Db	121	SYRQHTGVLKIVLWAVWVILAFVLNPGMILVSVESWKDEGS--ECEPGFSEWYILAIT	178		
Qy	181	AFLEPLLPVSLVYFVSQIYIWSLWKRGLSRCPHAGFIATSSRGTHSRRTGLACRTSL	240		
Db	179	SFLSFVIPVLVAVFNNIYWSLWKRDLHSLRCQSHPGLTAVSSNICGHSFGRLLSRRSL	238		
Qy	241	PGLPEPAASHSESPRGKSSLLVSLRTHMSGISITAPKVGSCRSFSPVHOREHVELLRG	300		
Db	239	SASTVEPASFSEQRKRSLLMFSRSTKQNSNTTASKMGSPSQSDSVLHOREHVELLRA	298		
Qy	301	RKLARSLAVLSAFAICWAPYCLFTIVLSTYRRGERPKSIWYSIAFWLQWNSLINPPLY	360		
Db	299	RRLAKSLAILLCVPAWCHAPYSLFTIVLSFYSSATGPKSVWYRIAFWLQWNSFNPPLY	358		
Qy	361	PLCHRRFQKAPWKILCVTKQPAPSQ--TQSVSS	391		
Db	359	PLCHKRFQKAPLKFICIKKQPLPQSHRSVS	390		
RESULT 9					
ID	AA053050 standard; protein; 390 AA.				
AC	AA053050;				
XX					
DT	26-MAR-2002 (first entry)				
DE	Human G protein-coupled receptor nGPCR-2067.				
XX	Human; nGPCR-2067; G protein-coupled receptor; 7TM receptor;				
KW	signal transduction; mental disorder; central nervous system disease;				
KW	metabolic disease; infection; HIV-1; HIV-2; pain; neurological disorder;				
KW	psychotic disorder; Huntington's disease; schizophrenia; migraine;				
KW	depression; anxiety; bipolar disorder; dementia; Alzheimer's disease;				
KW	Parkinson's disease; proliferative disorder; cancer; psoriasis;				
KW	benign prostatic hypertrophy; diabetes; dyslipidemia; obesity; anorexia;				
KW	thyroid disorder; cardiovascular disease; hypotension; hypertension;				
KW	thrombosis; myocardial infarction; cardiomyopathy; atherosclerosis;				
KW	inflammatory conditions; autoimmune disorder; rheumatoid arthritis;				
KW	hormonal disorder; renal failure; anti-HIV; analgesic; cytostatic;				
KW	antidiabetic; metabolic; hypertensive; hypotensive; thrombolytic;				
KW	cardiac; antiatherosclerotic; neuroleptic; antimigraine;				
KW	antiparkinsonian; tranquiliser; antidepressant; neuroprotective;				
KW	anticonvulsant; antinflammatory; antirheumatic; antiarthritic;				
KW	antipsoriatic; gene therapy; receptor.				
OS	Homo sapiens.				
XX					
PH	Location/Qualifiers				
FT	Domain	19..41	/label= Transmembrane_domain_1		
FT	Domain	52..74	/label= Transmembrane_domain_2		
FT	Domain	86..110	/label= Transmembrane_domain_3		
FT	Domain	128..146	/label= Transmembrane_domain_4		
FT	Domain	172..194			
FT	Domain				
/label= Transmembrane_domain_5					
305..326					
/label= Transmembrane_domain_6					
342..360					
/label= Transmembrane_domain_7					
WO200185793-A2.					
PD	15-NOV-2001.				
XX					
PF	08-MAY-2001; 2001WO-US014750.				
XX					
PR	08-MAY-2000; 2000US-0203108P.				
XX	(PHAA ) PHARMACIA & UPJOHN CO.				
XX					
PI	Lind P, Sejlitz T, Vogeli G, Wood LS;				
XX	WPI; 2002-062240/08.				
DR	N-PSDB; ABA02496.				
XX					
PT	New polynucleotide, useful for identifying modulator compounds which are				
PT	used for treating psoriasis, schizophrenia, diabetes, encodes the novel G				
PT	protein-coupled receptor (nGPCR) polypeptide (nGPCR-2067).				
XX	Claim 31; Page 63; 100pp; English.				
PS					
XX					
CC	This sequence represents a novel human G protein-coupled receptor (GPCR)				
CC	designated nGPCR-2067. Like all GPCRs, nGPCR-2067 has 7 putative				
CC	transmembrane domains and is involved in signal transduction. The				
CC	invention also relates to expression vectors and host cells comprising				
CC	nucleic acids encoding nGPCR-2067, to recombinant expression of nGPCR-				
CC	2067, to antibodies specific for nGPCR-2067, to drug screening methods				
CC	that use nGPCR-2067, and to modulators of nGPCR-2067 activity. nGPCR-2067				
CC	nucleic acid sequences may be used to isolate nGPCR-2067 allelic variants				
CC	and species homologues and may also be used in genetic mapping. The				
CC	invention also discloses the use of nGPCR-2067 nucleic acids in screening				
CC	for a predisposition to nGPCR-2067-associated hereditary mental				
CC	disorders, or for the diagnosis of these disorders. nGPCR-2067 nucleic				
CC	acids may additionally be used to generate transgenic animals, including				
CC	knockout animals, which may provide an insight into treating a variety of				
CC	human disorders, and may also be used in the design of antisense				
CC	molecules for suppressing expression of nGPCR-2067 in cells. nGPCR-2067,				
CC	and nGPCR-2067 modulators may be used to treat a wide variety of medical				
CC	conditions, particularly mental disorders, central nervous system				
CC	diseases, and metabolic diseases. Diseases that may be treated include				
CC	viral infections, particularly HIV-1 or HIV-2 infections; pain; central				
CC	nervous system, neurological and psychotic disorders such as Huntington's				
CC	disease, schizophrenia, migraine, depression, anxiety, bipolar disorder,				
CC	dementia, Alzheimer's disease, and Parkinson's disease; proliferative				
CC	disorders such as cancers, benign prostatic hypertrophy and psoriasis;				
CC	metabolic disorders such as diabetes, dyslipidaemia, obesity, and				
CC	anorexia; thyroid disorders; cardiovascular diseases such as hypotension,				
CC	hypertension, thrombosis, myocardial infarction, cardiomyopathies, and				
CC	atherosclerosis; inflammatory conditions; autoimmune disorders (e.g.,				
CC	rheumatoid arthritis); hormonal disorders; and renal failure				
XX	Sequence 390 AA;				
SQ					
Query Match		68.6%;	Score 1403.5;	DB 5;	Length 390;
Best Local Similarity		69.1%;	Pred. No. 1.7e-137;		
Matches		271;	Conservative	40;	Mismatches 78; Indels 3; Gaps 2;
Qy	1	MSENGTDLVPLTAQVPLAFMLSLAFITGNNAVILAFVADNRNLRHSYFFFLNLAIS	60		
Db	1	MPDNTSTINLSLSTRVTLAPFMSLVAFALMGNALVILAFVVDKNLRHSYFFFLNLAIS	60		
Qy	61	DFPVGVISIPLYIPHTLFPNNPGSGICMFWLITDYLLCTASVYSIVLSIDRYQSVNAV	120		
Db	61	DFPVGVISIPLYIPHTLFEWDFGKEICVFWLITDYLLCTASVYINVLISIDRYLSVNAV	120		
Qy	121	RYRAQHTGILKIVAQMAVWILAFVLNPGMILADSGNKNSTNTECEPGFVTEWYILAIT	180		

PI Wang S;  
 XX WPI; 2002-673827/72.  
 XX N-PSDB; ABW78739.  
 XX Novel mammalian histamine receptor polypeptide useful for identifying  
 PT agonist or antagonist for treating diseases such as inflammation, asthma,  
 PT stroke, migraine, rheumatoid arthritis, multiple sclerosis, psoriasis.  
 XX Claim 2; Page 16-17; 21pp; English.  
 XX The present sequence represents a histamine receptor. The polypeptide is  
 CC useful for identifying an agonist or antagonist of a mammalian histamine  
 CC receptor. It is useful as an antigen to elicit the production of  
 CC antibodies. The histamine receptor polypeptide and polynucleotide are  
 CC useful in the treatment and management of diseases such as inflammation,  
 CC asthma, allergy, atopic dermatitis, stroke, myocardial infection,  
 CC migraine, chronic obstructive pulmonary disease (COPD), rheumatoid  
 CC arthritis, multiple sclerosis, inflammatory bowel disease and psoriasis.  
 CC They are also useful for modulating intracellular second messenger  
 CC pathway activated through histamine receptors (cyclic-AMP, calcium,  
 CC inositol phosphate and mitogen activated protein (MAP) kinase), changes  
 CC in cellular growth rate, secretion of hormones, receptor-stimulated Ca2+  
 CC mobilization, mitogenic effects, etc  
 XX Sequence 390 AA;  
 SQ  
 Query Match : 68.6%; Score 1403.5; DB 5; Length 390;  
 Best Local Similarity 69.1%; Pred. No. 1.7e-137;  
 Matches 271; Conservative 40; Mismatches 78; Indels 3; Gaps 2;  
 Qy 1 MSENQDVLPLTAQVPLAFMLSLAPAITGNVAVILAFVADNLRHRSYFFLNLAIS 60  
 Db 1 MPDNTNINLSLSTRVTILAFPMISLVAFAIMLGNALVILAFVVDKNLRHRSYFFLNLAIS 60  
 Qy 61 DFFVGVISIPLYIPTLFFNPNPGSGICMFMLITDYLCTASVYSLVLSYDRYQSVNAV 120  
 Db 61 DFFVGVISIPLYIPTLFEWDFGKEICVFMLTDTLLCTASVYVILVLSYDRYLSVNAV 120  
 Qy 121 RYRAQHTGILKIVAQVAVVILAFVNGPMLASDSKNSNTNTECEPGFVTEWYILAIT 180  
 Db 121 SYRTQHTGVLKIVLAVVAVVILAFVNGPMLVSVESWKDEGS--ECEPGFSEWYILAIT 178  
 Qy 181 AFLBFLPVSLVYVFSVOIYVSLWKRGSLRCPHAGFIATSGTGHRSRTGLACRTSL 240  
 Db 179 SFLEFVPIVILVAVFYNNIYVSLWKDLHSLRCSQHPGLTAVSSNICGHSFGRLLSRRL 238  
 Qy 241 PGLKEPAASLHSESPRGKSSLLVSLRTHMSGSIITAPKVGSCFRCSESPVLHOREHVELLRG 300  
 Db 239 SASTEVPAFHSERQRKSSLMFSRTKMSNTTASKMGFSQSDSVLHOREHVELLRA 298  
 Qy 301 RKLARSLAVLSAFAICWAPYCLFTIVLSTYRRGERPKSIWYSTAFMLQWNSLINPLY 360  
 Db 299 RRLAKSLAILLGVFAVCWAPYSLFTIVLSFYSSATGPKSVYRIAFMLQWNSFNPLY 358  
 Qy 361 PLCHRRFOKAFWKILCVTKQAPSQ-TQSVSS 391  
 Db 359 PLCHKRFQAKFLKIFCKIKQPLPSQHSRSVSS 390  
 RESULT 12  
 AAM50564  
 ID AAM50564 standard; protein; 390 AA.  
 XX AC AAM50564;  
 XX 18-MAR-2002 (first entry)  
 XX Human histamine H4 receptor.  
 KW Histamine H4 receptor; human; antiasthmatic; antiallergenic;  
 KW antiinflammatory; cardiant; circulatory; antidiabetic; laxative;  
 KW diagnosis; Gene therapy.

XX Homo sapiens.  
 OS WO200192485-A1.  
 XX 06-DEC-2001.  
 XX 22-FEB-2001; 2001WO-US005914.  
 XX 31-MAY-2000; 2000US-0208260P.  
 XX (ORTH ) ORTHO-MCNEIL PHARM INC.  
 XX Lovenberg T, Liu C;  
 XX WPI; 2002-114339/15.  
 XX N-PSDB; AAI70980.  
 XX New mammalian histamine H4 receptor proteins and polynucleotides encoding  
 PT the proteins, useful in gene therapy for treating diseases where it is  
 PT beneficial to elevate mammalian histamine H4 receptor activity.  
 XX Claim 13; Fig 2; 92pp; English.  
 XX The present sequence is that of a human histamine receptor of the H4  
 CC subtype, as predicted from a cDNA clone isolated from a bone marrow cDNA  
 CC library. The invention provides mammalian (human, mouse, rat and guinea  
 CC pig) histamine H4 receptor nucleic acid molecules (see AAI70980-83) and  
 CC polypeptides (see AAM50564-67). The nucleic acids have been expressed in  
 CC recombinant host cells that produce active recombinant protein. The  
 CC pharmacology of known histamine ligands is demonstrated. Mammalian  
 CC histamine H4 receptor may be used in gene therapy for the treatment of  
 CC diseases where it is beneficial to elevate mammalian histamine H4  
 CC receptor activity. Recombinant protein is useful for identifying  
 CC modulators of the human histamine H4 receptor. Such modulators may be  
 CC useful for diagnosing, treating or preventing asthma, allergy,  
 CC inflammation, cardiovascular and cerebrovascular disorders, non-insulin  
 CC dependent diabetes mellitus, hyperglycemia, constipation, arrhythmia,  
 CC disorders of the neuroendocrine system, stress and spasticity  
 XX Sequence 390 AA;  
 SQ  
 Query Match : 68.6%; Score 1403.5; DB 5; Length 390;  
 Best Local Similarity 69.1%; Pred. No. 1.7e-137;  
 Matches 271; Conservative 40; Mismatches 78; Indels 3; Gaps 2;  
 Qy 1 MSENQDVLPLTAQVPLAFMLSLAPAITGNVAVILAFVADNLRHRSYFFLNLAIS 60  
 Db 1 MPDNTNINLSLSTRVTILAFPMISLVAFAIMLGNALVILAFVVDKNLRHRSYFFLNLAIS 60  
 Qy 61 DFFVGVISIPLYIPTLFFNPNPGSGICMFMLITDYLCTASVYSLVLSYDRYQSVNAV 120  
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 Qy 121 RYRAQHTGILKIVAQVAVVILAFVNGPMLASDSKNSNTNTECEPGFVTEWYILAIT 180  
 Db 121 SYRTQHTGVLKIVLAVVAVVILAFVNGPMLVSVESWKDEGS--ECEPGFSEWYILAIT 178  
 Qy 181 AFLBFLPVSLVYVFSVOIYVSLWKRGSLRCPHAGFIATSGTGHRSRTGLACRTSL 240  
 Db 179 SFLEFVPIVILVAVFYNNIYVSLWKDLHSLRCSQHPGLTAVSSNICGHSFGRLLSRRL 238  
 Qy 241 PGLKEPAASLHSESPRGKSSLLVSLRTHMSGSIITAPKVGSCFRCSESPVLHOREHVELLRG 300  
 Db 239 SASTEVPAFHSERQRKSSLMFSRTKMSNTTASKMGFSQSDSVLHOREHVELLRA 298  
 Qy 301 RKLARSLAVLSAFAICWAPYCLFTIVLSTYRRGERPKSIWYSTAFMLQWNSLINPLY 360  
 Db 299 RRLAKSLAILLGVFAVCWAPYSLFTIVLSFYSSATGPKSVYRIAFMLQWNSFNPLY 358  
 Qy 361 PLCHRRFOKAFWKILCVTKQAPSQ-TQSVSS 391  
 Db 359 PLCHKRFQAKFLKIFCKIKQPLPSQHSRSVSS 390





modulators of signal transduction for treating kidney disease, hyperlipidemia, obesity, dyslexia and cardiac myxoma.

Claim 26; Page 61; 78pp; English.

The present invention relates to a new G-protein coupled receptor (GPCR) polypeptide comprising greater than 70% amino acid sequence identity to the amino acid sequence of human GPCRs TGR62, TGR21, TGR130.1, TGR130.2, human TGR213 or TGR92, 80% amino acid sequence identity to mouse TGR18 or 90% amino acid sequence identity to human novel edg receptor protein, as defined in the specification. The GPCR covalently linked to a solid phase is useful for identifying a compound that modulates signal transduction. The identified compounds are useful for treating kidney disease, cerebral cavernous malformations, hyperlipidemia, obesity, dyslexia and cardiac myxoma. The molecules of the invention are useful for diagnosing disorders or conditions such as kidney-related conditions or diseases such as renal failure, nephritis, nephrotic syndrome, asymptomatic urinary abnormalities, renal tubule defects, hypertension and nephrolithiasis, liver-related disease or condition e.g. cirrhosis, infiltrations, lesions, functional disorders and jaundice and spleen-associated disorders or conditions e.g. splenic enlargement, immune disorders, blood disorders and others. Modulation of the polypeptide of the invention is useful to treat or prevent any of the above conditions or diseases. The present amino acid sequence represents the human GPCR TGR62 protein of the invention. This sequence is one of seven novel G protein coupled receptors of the invention (AAU74904-AAU74911).





GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 3, 2005, 01:39:17 ; Search time 158 Seconds  
(without alignments)  
964.157 Million cell updates/sec

Title: US-10-626-126-9

Perfect score: 2045

Sequence: 1 MSENNGTDVLPTRAQVPLAF.....WKILCVTKQAPAPSTQSVSS 391

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1745140 seqs, 389608008 residues

Total number of hits satisfying chosen parameters: 1745140

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	2045	100.0	391	16	US-10-626-445-9 Sequence 9, Appli
2	2045	100.0	391	17	US-10-626-126-9 Sequence 9, Appli
3	2045	100.0	391	17	US-10-626-398-9 Sequence 9, Appli
4	1735	84.8	391	16	US-10-626-445-8 Sequence 8, Appli
5	1735	84.8	391	17	US-10-626-126-8 Sequence 8, Appli
6	1735	84.8	391	17	US-10-626-398-8 Sequence 8, Appli
7	1403.5	68.6	390	9	US-09-812-216-2 Sequence 2, Appli
8	1403.5	68.6	390	9	US-09-910-411-2 Sequence 2, Appli
9	1403.5	68.6	390	10	US-09-875-076-14 Sequence 14, Appl
10	1403.5	68.6	390	10	US-09-876-252-14 Sequence 14, Appl
11	1403.5	68.6	390	10	US-09-852-165-2 Sequence 2, Appli

12	1403.5	68.6	390	10	US-09-891-138A-6	Sequence 6, Appli
13	1403.5	68.6	390	13	US-10-052-193-2	Sequence 2, Appli
14	1403.5	68.6	390	14	US-10-225-567A-629	Sequence 629, App
15	1403.5	68.6	390	14	US-10-272-983-14	Sequence 14, Appl
16	1403.5	68.6	390	14	US-10-354-769-2	Sequence 2, Appli
17	1403.5	68.6	390	14	US-10-393-807-14	Sequence 14, Appl
18	1403.5	68.6	390	15	US-10-417-820A-14	Sequence 14, Appl
19	1403.5	68.6	390	15	US-10-349-253A-2	Sequence 2, Appli
20	1403.5	68.6	390	16	US-10-696-673-2	Sequence 2, Appli
21	1403.5	68.6	390	16	US-10-723-955-14	Sequence 14, Appl
22	1403.5	68.6	390	16	US-10-782-596-14	Sequence 14, Appl
23	1403.5	68.6	390	16	US-10-737-619-2	Sequence 2, Appli
24	1403.5	68.6	390	16	US-10-626-445-2	Sequence 2, Appli
25	1403.5	68.6	390	17	US-10-684-206-20	Sequence 20, Appl
26	1403.5	68.6	390	17	US-10-616-088-2	Sequence 2, Appli
27	1403.5	68.6	390	17	US-10-626-126-2	Sequence 2, Appli
28	1403.5	68.6	390	17	US-10-626-398-2	Sequence 2, Appli
29	1398.5	68.4	390	14	US-10-290-078-27	Sequence 27, Appl
30	1236.5	60.5	389	16	US-10-626-445-10	Sequence 10, Appl
31	1236.5	60.5	389	17	US-10-626-126-10	Sequence 10, Appl
32	1236.5	60.5	389	17	US-10-626-398-10	Sequence 10, Appl
33	698	34.1	445	15	US-10-453-106-2	Sequence 2, Appli
34	698	34.1	445	17	US-10-735-963-2	Sequence 2, Appli
35	693	33.9	445	9	US-09-350-206-2	Sequence 2, Appli
36	693	33.9	445	9	US-03-349-755-2	Sequence 2, Appli
37	693	33.9	445	9	US-09-166-334-2	Sequence 2, Appli
38	693	33.9	445	14	US-10-282-958-2	Sequence 2, Appli
39	693	33.9	445	14	US-10-325-567A-549	Sequence 549, App
40	693	33.9	445	15	US-10-453-106-1	Sequence 1, Appli
41	693	33.9	445	16	US-10-727-021-7	Sequence 7, Appli
42	693	33.9	445	16	US-10-757-262-132	Sequence 132, App
43	693	33.9	445	17	US-10-735-963-1	Sequence 1, Appli
44	693	33.9	453	9	US-09-891-053-20	Sequence 20, Appl
45	693	33.9	453	17	US-10-759-463-20	Sequence 20, Appl

ALIGNMENTS

RESULT 1  
US-10-626-445-9  
; Sequence 9, Application US/10626445  
; Publication No. US20040248252A1  
; GENERAL INFORMATION:  
; APPLICANT: Lovenberg, Timothy  
; APPLICANT: Liu, Changlu  
; TITLE OF INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Subtype  
; FILE REFERENCE: PRD-0032  
; CURRENT APPLICATION NUMBER: US/10/626,445  
; PRIOR FILING DATE: 2003-07-23  
; PRIOR APPLICATION NUMBER: 09/790,849  
; PRIOR FILING DATE: 2001-02-22  
; PRIOR APPLICATION NUMBER: 60/208,260  
; PRIOR FILING DATE: 2000-05-31  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 9  
; LENGTH: 391  
; TYPE: PRT  
; ORGANISM: Rattus rattus  
US-10-626-445-9

Query Match	100.0%	Score	2045	DB	16	Length	391
Best Local Similarity	100.0%	Pred. No.	1.1e-183				
Matches	391	Conservative	0	Mismatches	0	Indels	0
Gaps	0						
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Db	1	MSENNGTDVLPTRAQVPLAFSLAFAITGNNAVILAFVADRNLRLHRSNYFFFLNLAIS	60				
Qy	61	DFFGVGSIPILYIPHTLFWNNPGSGICMFWLITDYLCTASVYSIVLISVDRYQSVSNV	120				
Db	61	DFFGVGSIPILYIPHTLFWNNPGSGICMFWLITDYLCTASVYSIVLISVDRYQSVSNV	120				

QY 121 RYRAQHTGILKIVAQMVAWVILAFVNGPMLASDSWKNSTNTECEPGFVTEWYILAIT 180  
DB 121 RYRAQHTGILKIVAQMVAWVILAFVNGPMLASDSWKNSTNTECEPGFVTEWYILAIT 180  
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QY 241 PGLKEPAASHSES PRGKSSLLVSLRTHMSGSIIFKVGSCFCSSES PVLHQREHVELLRG 300  
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QY 301 RKLARS LVLASAFACWAPYCLFTIVLSTYRRGERPKSIWYSIAFWLQWNSLINPPLY 360  
DB 301 RKLARS LVLASAFACWAPYCLFTIVLSTYRRGERPKSIWYSIAFWLQWNSLINPPLY 360  
QY 361 PLCHRRFQKAFWKILCVTKQAPSPQTSQSVSS 391  
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## RESULT 2

US-10-626-126-9  
; Sequence 9, Application US/10626126  
; Publication No. US20050074770A1  
; GENERAL INFORMATION:  
; APPLICANT: Lovenberg, Timothy  
; APPLICANT: Liu, Changlu  
; TITLE OF INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Subtype  
; FILE REFERENCE: PRD-0033  
; CURRENT APPLICATION NUMBER: US/10/626,126  
; PRIOR FILING DATE: 2003-07-23  
; PRIOR APPLICATION NUMBER: 09/790,849  
; PRIOR FILING DATE: 2001-02-22  
; PRIOR APPLICATION NUMBER: 60/208,260  
; PRIOR FILING DATE: 2000-05-31  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 9  
; LENGTH: 391  
; TYPE: PRT  
; ORGANISM: Rattus rattus  
US-10-626-126-9

Query Match 100.0%; Score 2045; DB 17; Length 391;  
Best Local Similarity 100.0%; Pred. No. 1.1e-183;  
Matches 391; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MSESNGTDVLP LTAQVPLAFMSLLAFATITGNNAVILAFVADRNLRHRSNYFFLNLAIS 60  
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DB 301 RKLARS LVLASAFACWAPYCLFTIVLSTYRRGERPKSIWYSIAFWLQWNSLINPPLY 360

QY 361 PLCHRRFQKAFWKILCVTKQAPSPQTSQSVSS 391  
DB 361 PLCHRRFQKAFWKILCVTKQAPSPQTSQSVSS 391

## RESULT 3

US-10-626-398-9  
; Sequence 9, Application US/10626398  
; Publication No. US20050074841A1  
; GENERAL INFORMATION:  
; APPLICANT: Lovenberg, Timothy  
; APPLICANT: Liu, Changlu  
; TITLE OF INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Subtype  
; FILE REFERENCE: PRD-0034  
; CURRENT APPLICATION NUMBER: US/10/626,398  
; PRIOR FILING DATE: 2003-07-23  
; PRIOR APPLICATION NUMBER: 09/790,849  
; PRIOR FILING DATE: 2001-02-22  
; PRIOR APPLICATION NUMBER: 60/208,260  
; PRIOR FILING DATE: 2000-05-31  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 9  
; LENGTH: 391  
; TYPE: PRT  
; ORGANISM: Rattus rattus  
US-10-626-398-9

Query Match 100.0%; Score 2045; DB 17; Length 391;  
Best Local Similarity 100.0%; Pred. No. 1.1e-183;  
Matches 391; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 DFFVGVISIPLYIPHTL FNNWPGSGICMFMLITDYLLCTASVYSIVILSYDRYQSVSNV 120  
DB 61 DFFVGVISIPLYIPHTL FNNWPGSGICMFMLITDYLLCTASVYSIVILSYDRYQSVSNV 120  
QY 121 RYRAQHTGILKIVAQMVAWVILAFVNGPMLASDSWKNSTNTECEPGFVTEWYILAIT 180  
DB 121 RYRAQHTGILKIVAQMVAWVILAFVNGPMLASDSWKNSTNTECEPGFVTEWYILAIT 180  
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DB 181 AFLEFLLPVSLVYVFSQIYWSLWKGSLSRCPSHAGFIATSRGTGHSRRTGLACRTSL 240  
QY 241 PGLKEPAASHSES PRGKSSLLVSLRTHMSGSIIFKVGSCFCSSES PVLHQREHVELLRG 300  
DB 241 PGLKEPAASHSES PRGKSSLLVSLRTHMSGSIIFKVGSCFCSSES PVLHQREHVELLRG 300  
QY 301 RKLARS LVLASAFACWAPYCLFTIVLSTYRRGERPKSIWYSIAFWLQWNSLINPPLY 360  
DB 301 RKLARS LVLASAFACWAPYCLFTIVLSTYRRGERPKSIWYSIAFWLQWNSLINPPLY 360  
QY 361 PLCHRRFQKAFWKILCVTKQAPSPQTSQSVSS 391  
DB 361 PLCHRRFQKAFWKILCVTKQAPSPQTSQSVSS 391

## RESULT 4

US-10-626-445-8  
; Sequence 8, Application US/10626445  
; Publication No. US20040248252A1  
; GENERAL INFORMATION:  
; APPLICANT: Lovenberg, Timothy  
; APPLICANT: Liu, Changlu  
; TITLE OF INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Subtype  
; FILE REFERENCE: PRD-0032  
; CURRENT APPLICATION NUMBER: US/10/626,445  
; CURRENT FILING DATE: 2003-07-23  
; PRIOR APPLICATION NUMBER: 09/790,849

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241 PGLKESAARSHSESPPRKSSILVSLRTHMNSSIIAFAKVGSFWRSESAALQRQEYAELLRG 300
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RESULT 6
US-10-6266-398-8
; Sequence 8, Application US/106266398
; Publication No. US20050074841A1
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Liu, Changlu
; TITLE OF INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Sub
; FILE REFERENCE: PRD-0034
; CURRENT APPLICATION NUMBER: US/10/626,398
; CURRENT FILING DATE: 2003-07-23
; PRIOR APPLICATION NUMBER: 09/790,849
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/208,260
; PRIOR FILING DATE: 2000-05-31

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; SOFTWARE: PATENTCIN VERSION 3.2
; SEQ ID NO 8
; LENGTH: 391
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-626-398-8

Query Match      84.8%; Score 1735; DB 17; Length 391;
Best Local Similarity 84.7%; Pred. No. 1.6e-154;
Matches 331; Conservative 17; Mismatches 43; Indels 0; Gaps 0

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Db 1 M S E S N S T G I L P P A A Q V P L A F L M S S F A F A I M V G N A V V I L A F V D R N L R H R S N Y F F L N L A I S 60

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      ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 61 D F L V G L I S I P L Y I P H V L F N N N F G S G I C M F W I L T D Y L L C T A S Y S V I N V I L I S Y D R Y Q S V S N A V 120

Qy 121 R Y R A Q T G I L K I V A Q M A V A W I L A F L V N G P M I L A S D S W K N S T N T E C E P G F V T E W Y I L A T 180
      ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 121 S Y R A Q T G I M K I V A Q M A V A W I L A F L V N G P M I L A S D S W K N S T N T K D C E P G F V T E W Y I L T I T 180

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      ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
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Qy 241 P G L K E P A A S L H S E S P R K S S L L V S L R T H M S G S I T A F K V G S F C R S R S P V L H Q R E H V E L L R G 300
      ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 241 P G L K E A A S R H S E S P R R K S S T L V S L R T H M S S I T A F K V G S F W R S S A A L R O R E Y A E L L R G 300

```

[illegible]

## RESULT 7

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US-09-812-216-2
; Sequence 2, Application US/09/812216
; Publication No. US20020098539A1
; GENERAL INFORMATION:
; APPLICANT: Behan, Jang Xu
; APPLICANT: Hedrick, Joseph A.
; APPLICANT: Laz, Thomas M.
; APPLICANT: Monsma, Frederick J. Jr.
; APPLICANT: Morse, Kelley L.
; APPLICANT: Umland, Shelby P.
; APPLICANT: Wang, Suke
; TITLE OF INVENTION: Histamine receptor
; FILE REFERENCE: CN01069
; CURRENT APPLICATION NUMBER: US/09/812,216
; CURRENT FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: 09/414,010
; PRIOR FILING DATE: 1999-10-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-812-216-2

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Query Match	68.6t;	Score 1403.5;	DB 9;	Length 390;
Best Local Similarity	69.1t;	Pred. No. 2.6e-123;		
Matches 271;	Conservative 40;	Mismatches 78;	Indels 3;	Gaps 2;
Qy	1	MSBNGTDLVPLTAQVPLAFMLSLAFATITGNAAVILAFVADRNLRHSRNPFLNLAI	60	
Db	1	MPDNTSINISLRVTLAFPMSLVAFMILGNALVILAFVDDKNLRHSYFFNLAI	60	
Qy	61	DFPVGVISIPLYIPHTLTFNNPNSGGICMFWLITDYLCTASVYSIVLISYDRYOSGNV	120	
Db	61	DFPVGVISIPLYIPHTLTFEWDGKEICVFWLTDTDYLLCTASVYIVLISYDRYLSVSNV	120	
Qy	121	RYRAQHTGILKIVAQMAVAILAFVLNPGMILASDSWKNSTNTCECPGPTVEYILAIT	180	
Db	121	SYRTQHTGVLKIVTLMAVAVMLAFVLNPGMILVSESWKDEGS--ECSPGFSEWYILAIT	178	
Qy	181	AFLEFLLPVSLIVVYFSVOIYWSLWKRGSLRCPSHAGFIATSSRGTHGSRRTGLACTSL	240	
Db	179	SFLFEVIPVLIVAFNNIYWSLWKRDHLRSCQSHPGILTAVSSNICGHSFGRLLSSRSL	238	
Qy	241	PGLKEPAASLHSESPPRGKSSLLVSLRTHMSGSIITAFVGSFCRSESPLVHOREHVLLRG	300	
Db	239	SASTEVPASPHERQRRKSSLMFSSRTKMNSTIASKGSFSDQSVALHOREHVELLA	298	
Qy	301	RKLARSILAVLLSAFAICWAPYCLTIVLSTVYRRGERPKSIWYSIAFWLQWNSLINPELY	360	
Db	299	RRLAKSLAILLCVFAVCWAPYSLTIVLSFYSSATGPKSVWYRTAFWLOWFNSVPNELLY	358	
Qy	361	PLCHRRFOKAPKWLICVTQKPAQSQ--TQSVSS	391	
Db	359	PLCHRKFOKAPLKIFCIKKQPLPQSHGRSVSS	390	

## RESULT 8

US-09-910-411-2  
; Sequence 2, Application US/09910411  
; Patent No. US20020137054A1

```

; GENERAL INFORMATION:
; APPLICANT: Bergsma, Derk
; APPLICANT: Fitzgerald, Laura
; APPLICANT: Li, Xiatong
; APPLICANT: Michalovich, David
; APPLICANT: Zhu, Yuan
; TITLE OF INVENTION: AXOR35, A G-Protein Coupled Receptor
; FILE REFERENCE: GP70655-2C1
; CURRENT APPLICATION NUMBER: US/09/910,411
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: 09/693,761
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 09/497,790
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/431,898
; PRIOR FILING DATE: 1999-11-02
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-910-411-2

Query Match 68.6%; Score 1403.5; DB 9; Length :
Best Local Similarity 69.1%; Pred. No. 2.6e-123;
Matches 271; Conservative 40; Mismatches 78; Indels

Qy 1 MSENGTDVLPETAQVPLAFMLSLAPAITIGNAVVILAFVADRNLRHRR
Db 1 MPDNTSTNLSTRVTLAFPMSLVAFATMLGNALVILAFVVDNLRHRR
Qy 61 DFFVGVISIPYIPHTLFNNPMSGICMPWLITDYLCTASVYSIVLIS
Db 61 DFFVGVISIPYIPHTLEWDEKELCVFWLTTDYLCTASVYIVLIS
Qy 121 RYRAQHTGILKIVAQMVAVWILAFVLVNGPMILASDSWKSTNTECEPGG
Db 121 SYRTQHTGVKIVTLWVAVVILAFVLVNGPMILVSBWMKDEGS--ECEPGG
Qy 181 AFLFPLLPVSLVVVPSVQIYNSLWKRGSLRSCPSHAGFIATSSRGTHGHS
Db 179 SFLEFVIVILVAYENMNIYNSLWKRDHLSRCQSHFGLTAVSSNICGHS
Qy 241 PGLKEPAASLHSESPRGKSSLVLSRLTHMSGSIAPKVGSCFCSSEPVLA
Db 239 SASTEVPASFHSERQRRKSSLMFSFRKTNNSTIASKMGSPSOSDVALL
Qy 301 RKLARSLAVLSAFAICWAPYCLFTIVLSTYRRGERPKSIWYGIAPFWLQ
Db 299 RRLAKSLAILLGVFACVWAPYSLFTIVLSFYSSATGPKSVWYIAPFWLQ
Qy 361 PLCHRRFQAFKWLICVTNKQAPSQ--TQSVSS 391
Db 359 PLCHKRFQAFKLFKCIKKQPLPSQHSRSVSS 390

RESULT 9
US-09-875-076-14
; Sequence 14, Application US/09875076
; Publication No. US20030017528A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Dang, Huong T.
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
; FILE REFERENCE: AREN0050
; CURRENT APPLICATION NUMBER: US/09/875,076
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 09/417,044
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 60/120,416

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; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,851
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/123,946
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,949
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/136,436
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,437
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,439
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,567
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/137,127
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/137,131
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/141,448
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: 60/156,653
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,633
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,555
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,634
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/157,280
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,294
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,281
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,293
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,282
; PRIOR FILING DATE: 1999-10-01
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-875-076-14

Query Match 68.6%; Score 1403.5; DB 10; Length 390;
Best Local Similarity 69.1%; Pred. No. 2.6e-123;
Matches 271; Conservative 40; Mismatches 78; Indels 3; Gaps 2;

Qy 1 MSEGNDVLP LTAQVPLAFMLSLAPAITTIGNAVVILAFVADRLNRHSYFFFLNLAIS 60
Db 1 MPDNTSINLSLSTRVTLAFMSVAFAPMLGNALVILAFVVDKRLNRHSYFFFLNLAIS 60

Qy 61 DFFVGVISIPLYIPHTLFFNNMPSGICMFWLITDYLLCTASVYIVLSYDRYSQSVNAV 120
Db 61 DFFVGVISIPLYIPHTLFEWDFGKEICVFWLTTDYLLCTASVYIVLSYDRYSQSVNAV 120

Qy 121 RYRQHTGILKIVAQWAVVILAFVLNCPMLTASDSKWNSTNTECEPGFTWEVILAIT 180
Db 121 SYRTQHTGVKIVTLMAVAVVILAFVLNCPMLTASDSKWNSTNTECEPGFTWEVILAIT 178

Qy 181 AFLEPLPVSLVYVFSVOIYWSLWKRGLSRCPSHAGFIATSSRGTGHSRRTGLACRTSL 240
Db 179 SFLEFVIVLIVAFNMNIYWSLWKRDLHSLRCQHPGLTAVSSNICGHSFGRLSRRSL 238

Qy 241 PGLKEPAASHSESPRGKSSLLVSLRTHMSGIIAFKVGSFCRSESPVLHQREHVELLRG 300
Db 239 SASTEVPASFSRQRKRKSSLMFSSRTQWNTNTIASKMGFSQSDSVLHQREHVELLRA 298

Qy 301 RKLARSLAVLSAFACWAPYCLFTTIVLSTVRGERPKSIWYSIAFWLQWNSFNPLLY 360
Db 301 RKLARSLAVLSAFACWAPYCLFTTIVLSTVRGERPKSIWYSIAFWLQWNSFNPLLY 360

Db 299 RRLAKSLAILLGVFAVCWAPYSLETLIVLSFYSSATGPKSVWYRIAFWLQWNSFNPLLY 358
Qy 361 PLCHRRFQKAFWKILCVTKQPAPSQ-TQSVSS 391
Db 359 PLCHKRQKAFKIFCIKKQPLPSQHSRSVSS 390

RESULT 10
US-09-876-252-14
; Sequence 14, Application US/09876252
; Publication No. US20030018182A1
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Lehmann-Bruinsma, Karin
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Lowitz, Kevin P.
; APPLICANT: Lin, I-Lin
; APPLICANT: Dang, Huong T.
; APPLICANT: Chen, Ruoping
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: Non-Endogenous Constitutively Activated Human G Protein Coupled Rec
; FILE REFERENCE: AREN-0054
; CURRENT APPLICATION NUMBER: US/09/876,252
; CURRENT FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 09/416,760
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: 60/110,060
; PRIOR FILING DATE: 1998-11-27
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,852
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/109,213
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: 60/123,944
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,945
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,948
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,951
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,946
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,949
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/152,524
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: 60/151,114
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: 60/108,029
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: 60/136,436
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,439
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,567
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/137,127
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/137,131
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/141,448
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: 60/136,437
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/156,555
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,634
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,653

```

; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/157,280
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,294
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,281
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,282
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/156,633
; PRIOR FILING DATE: 1999-09-29
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-876-252-14

Query Match
Best Local Similarity 68.6%; Score 1403.5; DB 10; Length 390;
Matches 271; Conservative 40; Mismatches 78; Indels 3; Gaps 2;

QY 1 MSBSNGTDVLPATAQVPLAFMSLLAPAITIGNAVVILAFVADRNLRHRSNYFFLNLAIS 60
DB 1 MPDNTNINLSLSTRVTLAFPMISLVAFIMLGNALVILAFVVDKNLRHRSNYFFLNLAIS 60
QY 61 DFFVGVISIPLYIPHTLFWNNPGSGICMFWLIITDYLLCTASVYSIVILISYDRYQSVSNV 120
DB 61 DFFVGVISIPLYIPHTLFEWDFGKEICVFWLTDDYLLCTASVYNIVILISYDRYLSVSNV 120
QY 121 RYRAQHTGILKIIVAVVAVVILAFVNGPMLASDSWKNSTNTEECPEGFWTWYILAIT 180
DB 121 SYRTOHTGVLIKIVTLMVAVVWLAFVNGPMLVSESWKDEGS--ECPEGPFSEWYILAIT 178
QY 181 AFLEFLLPVSLVYVFSQIYIWSLWKRGLSRCPSHAGFIATSSRGTHGSRRTGLACRTSL 240
DB 179 SFLEFVLPVILVAYFNNIYWSLWKRDLHRCQHPGLTAVSSNICHSFGRLSRRSL 238
QY 241 PGLKEPAASLHSPRCKSLLVSLRTHMSGSIIFKVGSCFRCSESPVLHQREHVELLRG 300
DB 239 SASTEVPAFSPHSEQRKRSKSLMFSRTKMSNTIASKMGFSQSDSVALHQREHVELLRA 298
QY 301 RKLARSLAVLSAFAICWAPYCLFTIVLSTYRGERPKSIWYSIAFWLQWNSLINPFY 360
DB 299 RRLAKSLAILGVFAVCWAPYSLETTIVLSFYSSATGPKSVYRIAFWLOWFNSFVNPLLY 358
QY 361 PLCHRRFQKAFWKILCVTKOPAPSQ--TQSVSS 391
DB 359 PLCHKRQKAFKIFCIKKQPLPSQHSRSVSS 390

RESULT 12
US-09-891-138A-6
; Sequence 6, Application US/09891138A
; Publication No. US20030083245A1
; GENERAL INFORMATION:
; APPLICANT: Lin, Daniel Chi-Hong
; APPLICANT: Zhao, Jiagang
; APPLICANT: Chen, Jin-Long
; APPLICANT: Cutler, Gene
; APPLICANT: Tularik Inc.
; TITLE OF INVENTION: No. US20030083245A1e1 Receptors
; FILE REFERENCE: 018781-006210US
; CURRENT APPLICATION NUMBER: US/09/891,138A
; CURRENT FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: US 60/213,461
; PRIOR FILING DATE: 2000-06-23
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human TGR62 G-protein coupled receptor (GPCR)
US-09-891-138A-6

Query Match
Best Local Similarity 68.6%; Score 1403.5; DB 10; Length 390;
Matches 271; Conservative 40; Mismatches 78; Indels 3; Gaps 2;

QY 1 MSBSNGTDVLPATAQVPLAFMSLLAPAITIGNAVVILAFVADRNLRHRSNYFFLNLAIS 60
DB 1 MPDNTNINLSLSTRVTLAFPMISLVAFIMLGNALVILAFVVDKNLRHRSNYFFLNLAIS 60
QY 61 DFFVGVISIPLYIPHTLFWNNPGSGICMFWLIITDYLLCTASVYSIVILISYDRYQSVSNV 120
DB 61 DFFVGVISIPLYIPHTLFEWDFGKEICVFWLTDDYLLCTASVYNIVILISYDRYLSVSNV 120
QY 121 RYRAQHTGILKIIVAVVAVVILAFVNGPMLASDSWKNSTNTEECPEGFWTWYILAIT 180
DB 121 SYRTOHTGVLIKIVTLMVAVVWLAFVNGPMLVSESWKDEGS--ECPEGPFSEWYILAIT 178
QY 181 AFLEFLLPVSLVYVFSQIYIWSLWKRGLSRCPSHAGFIATSSRGTHGSRRTGLACRTSL 240
DB 179 SFLEFVLPVILVAYFNNIYWSLWKRDLHRCQHPGLTAVSSNICHSFGRLSRRSL 238
QY 241 PGLKEPAASLHSPRCKSLLVSLRTHMSGSIIFKVGSCFRCSESPVLHQREHVELLRG 300
DB 239 SASTEVPAFSPHSEQRKRSKSLMFSRTKMSNTIASKMGFSQSDSVALHQREHVELLRA 298
QY 301 RKLARSLAVLSAFAICWAPYCLFTIVLSTYRGERPKSIWYSIAFWLQWNSLINPFY 360
DB 299 RRLAKSLAILGVFAVCWAPYSLETTIVLSFYSSATGPKSVYRIAFWLOWFNSFVNPLLY 358
QY 361 PLCHRRFQKAFWKILCVTKOPAPSQ--TQSVSS 391
DB 359 PLCHKRQKAFKIFCIKKQPLPSQHSRSVSS 390

RESULT 11
US-09-852-165-2
; Sequence 2, Application US/09852165
; Publication No. US20030032784A1
; GENERAL INFORMATION:
; APPLICANT: Lind, Peter
; APPLICANT: Sejlitz, Torsten
; APPLICANT: Vogeli, Gabriel
; APPLICANT: Wood, Linda S.
; TITLE OF INVENTION: No. US20030032784A1e1 G Protein-Coupled Receptors
; FILE REFERENCE: 00231regUS
; CURRENT APPLICATION NUMBER: US/09/852,165
; CURRENT FILING DATE: 2001-05-08
; PRIOR APPLICATION NUMBER: US9N 60/203,108
; PRIOR FILING DATE: 2000-05-08
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapiens

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Qy 121 RYRAQHTGILKIVAQVAVWILAFVNGPMLASDSWKNSTNTBECBPGFVTEWYILAIT 180
Db 121 SYRTQHTGVLKIVTLMAVAVWVLAFLVNGPMTLVSESMKDEGS--ECEPGFFSEWYILAIT 178
Qy 181 AFLEFLLPVSLVYVFSVOIYWSLWKRGSLSRCPSHAGFIATSRGTGHSRRTGLACRTSL 240
Db 179 SFLEFVPIVLVAFVNNIYWSLWKRDLHSCQHPGLTAVSSNICGHSFGRLSRRSL 238
Qy 241 PGLKEPAASHSESPRGKSSLLVSLRTHMSGIIAFKVGSCRSSESPVLHQHREHVELLRG 300
Db 239 SASTEVPAFSEHSESPRGKSSLLVSLRTHMSGIIAFKVGSCRSSESPVLHQHREHVELLRG 298
Qy 301 RKLARSALLSFAIACWAPYCLTIVLSTYRRGERPKSIWYSIAFWLQWNSLINPLY 360
Db 299 RRLAKSAILLGVFAVCWAPYSLFTIVLSFYSSATGPKSVWYRIAFWLQWNSFVNPLY 358
Qy 361 PLCHRRFOKAFWKILCVTKQAPSQ-TQSVSS 391
Db 359 PLCHRRFOKAFWKILCVTKQAPSQ-TQSVSS 390
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RESULT 13
US-10-052-193-2
; Sequence 2, Application US/10052193
; Publication No. US20020132755A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer, Inc.
; TITLE OF INVENTION: HISTAMINE RECEPTOR ANTAGONISTS
; FILE REFERENCE: PC10963A
; CURRENT APPLICATION NUMBER: US/10/052.193
; CURRENT FILING DATE: 2002-01-17
; PRIOR FILING DATE: 2001-01-17
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-052-193-2
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Query Match 68.6%; Score 1403.5; DB 13; Length 390;
Best Local Similarity 63.1%; Pred. No. 2.6e-123;
Matches 271; Conservative 40; Mismatches 78; Indels 3; Gaps 2;

Qy 1 MSEGNGTDVLP LTAQVPLAFMLSLAFAITGNNAVILAFVADRNLRHRSYFFLNLAIS 60
Db 1 MPDTNSTINLSLSTRVILAFPMSLVAFALMGNALVILAFVVDKNLRHRSYFFLNLAIS 60
Qy 61 DFFVGVISIPLYIPIHTLFNNPNPGSGICMFWLITDYLCTASVYISIVLSYDRYQSVNAV 120
Db 61 DFFVGVISIPLYIPIHTLFENDFGKEICVFWLTTDYLCTASVYINVLISYDRYLSVNAV 120
Qy 121 RYRAQHTGILKIVAQVAVWILAFVNGPMLASDSWKNSTNTBECBPGFVTEWYILAIT 180
Db 121 SYRTQHTGVLKIVTLMAVAVWVLAFLVNGPMTLVSESMKDEGS--ECEPGFFSEWYILAIT 178
Qy 181 AFLEFLLPVSLVYVFSVOIYWSLWKRGSLSRCPSHAGFIATSRGTGHSRRTGLACRTSL 240
Db 179 SFLEFVPIVLVAFVNNIYWSLWKRDLHSCQHPGLTAVSSNICGHSFGRLSRRSL 238
Qy 241 PGLKEPAASHSESPRGKSSLLVSLRTHMSGIIAFKVGSCRSSESPVLHQHREHVELLRG 300
Db 239 SASTEVPAFSEHSESPRGKSSLLVSLRTHMSGIIAFKVGSCRSSESPVLHQHREHVELLRG 298
Qy 301 RKLARSALLSFAIACWAPYCLTIVLSTYRRGERPKSIWYSIAFWLQWNSLINPLY 360
Db 299 RRLAKSAILLGVFAVCWAPYSLFTIVLSFYSSATGPKSVWYRIAFWLQWNSFVNPLY 358
Qy 361 PLCHRRFOKAFWKILCVTKQAPSQ-TQSVSS 391
Db 359 PLCHRRFOKAFWKILCVTKQAPSQ-TQSVSS 390
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RESULT 14
US-10-225-567A-629
; Sequence 629, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burmer, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225.567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 629
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-629
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Query Match 68.6%; Score 1403.5; DB 14; Length 390;
Best Local Similarity 69.1%; Pred. No. 2.6e-123;
Matches 271; Conservative 40; Mismatches 78; Indels 3; Gaps 2;

Qy 1 MSEGNGTDVLP LTAQVPLAFMLSLAFAITGNNAVILAFVADRNLRHRSYFFLNLAIS 60
Db 1 MPDTNSTINLSLSTRVILAFPMSLVAFALMGNALVILAFVVDKNLRHRSYFFLNLAIS 60
Qy 61 DFFVGVISIPLYIPIHTLFNNPNPGSGICMFWLITDYLCTASVYISIVLSYDRYQSVNAV 120
Db 61 DFFVGVISIPLYIPIHTLFENDFGKEICVFWLTTDYLCTASVYINVLISYDRYLSVNAV 120
Qy 121 RYRAQHTGILKIVAQVAVWILAFVNGPMLASDSWKNSTNTBECBPGFVTEWYILAIT 180
Db 121 SYRTQHTGVLKIVTLMAVAVWVLAFLVNGPMTLVSESMKDEGS--ECEPGFFSEWYILAIT 178
Qy 181 AFLEFLLPVSLVYVFSVOIYWSLWKRGSLSRCPSHAGFIATSRGTGHSRRTGLACRTSL 240
Db 179 SFLEFVPIVLVAFVNNIYWSLWKRDLHSCQHPGLTAVSSNICGHSFGRLSRRSL 238
Qy 241 PGLKEPAASHSESPRGKSSLLVSLRTHMSGIIAFKVGSCRSSESPVLHQHREHVELLRG 300
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Qy 301 RKLARSALLSFAIACWAPYCLTIVLSTYRRGERPKSIWYSIAFWLQWNSLINPLY 360
Db 299 RRLAKSAILLGVFAVCWAPYSLFTIVLSFYSSATGPKSVWYRIAFWLQWNSFVNPLY 358
Qy 361 PLCHRRFOKAFWKILCVTKQAPSQ-TQSVSS 391
Db 359 PLCHRRFOKAFWKILCVTKQAPSQ-TQSVSS 390
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RESULT 15
US-10-272-983-14
; Sequence 14, Application US/10272983
; Publication No. US20030148450A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Dang, Huang T.
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
; FILE REFERENCE: AREN0050
; CURRENT APPLICATION NUMBER: US/10/272.983
; CURRENT FILING DATE: 2002-10-17
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 60/109,213
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GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: August 5, 2005, 12:29:04 ; Search time 4456 Seconds

(without alignments)  
4251.793 Million cell updates/sec

Title: US-10-626-126-9

Perfect score: 2045

Sequence: 1 MSENSTGTVLPLTAQVPLAF.....WKILCVTKQPAPSTQTSVSS 391

Scoring table:

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Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-DB=GenEmbl -QPMT=fastap -SUPFI=rcse -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR SCORES=ptc -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODES=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000  
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Database :

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2: gb.htg.\*  
3: gb.in.\*  
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5: gb.ov.\*  
6: gb.pat.\*  
7: gb.ph.\*  
8: gb.pl.\*  
9: gb.pr.\*  
10: gb.ro.\*  
11: gb.sts.\*  
12: gb.sy.\*  
13: gb.un.\*  
14: gb.vi.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2034	99.5	1593	10 AF358860	AF358860 Rattus no
2	1742	85.2	1538	10 AF358859	AF358859 Mus muscu
3	1434	70.1	236694	2 AC118386	AC118386 Rattus no
4	1405.5	68.7	1173	9 AY008280	AY008280 Homo sapi

5	1403.5	68.6	1173	6	AR142850	Sequence
6	1403.5	68.6	1173	6	AR391860	Sequence
7	1403.5	68.6	1173	6	AX109119	Sequence
8	1403.5	68.6	1173	6	AX139113	Sequence
9	1403.5	68.6	1173	6	AX301763	Sequence
10	1403.5	68.6	1173	6	BD015847	Novel pol
11	1403.5	68.6	1173	9	AF307973	Homo sapi
12	1403.5	68.6	1173	9	AF325356	Homo sapi
13	1403.5	68.6	1173	9	AF329449	Homo sapi
14	1403.5	68.6	1173	9	AY136745	Homo sapi
15	1403.5	68.6	1173	9	HSA298292	Homo sapi
16	1403.5	68.6	1266	6	AX376577	Sequence
17	1403.5	68.6	1300	6	AX301229	Sequence
18	1403.5	68.6	1312	6	BD095598	Novel gua
19	1403.5	68.6	1312	9	AB045370	Homo sapi
20	1403.5	68.6	1316	9	BC069136	Homo sapi
21	1403.5	68.6	1369	6	AX549343	Sequence
22	1403.5	68.6	1369	9	AF312230	Homo sapi
23	1398.5	68.4	1227	6	BD097512	Novel gua
24	1398.5	68.4	1265	9	AB044934	Homo sapi
25	1328.5	65.0	1291	4	AB053300	Sub scrof
26	1237.5	60.5	1451	10	AF358858	AF358858 Cavia por
27	1210.5	59.2	199837	10	AC131672	AC131672 Mus muscu
28	937	45.8	140555	9	AC007922	Homo sapi
29	937	45.8	168206	2	AC009668	Homo sapi
30	937	45.8	167296	2	AF002507	Homo sapi
31	937	45.8	169144	9	AC090244	Homo sapi
32	937	45.8	184938	2	AF002476	Homo sapi
33	937	45.8	193779	2	AP001327	Homo sapi
34	704.5	34.4	1600	9	AY231164	Macaca mu
35	703.5	34.4	1249	10	AF267538	Cavia por
36	697.5	34.1	1339	10	AF267537	Cavia por
37	693	33.9	1335	6	AR104202	Sequence
38	693	33.9	1335	6	AR135733	Sequence
39	693	33.9	1335	6	BD235873	Isolated
40	693	33.9	1335	6	AR217195	Sequence
41	693	33.9	1335	6	BD086286	G protein
42	693	33.9	1338	9	AF321910	Homo sapi
43	693	33.9	1362	9	AB019000	Homo sapi
44	693	33.9	2050	6	E39824	Novel guano
45	693	33.9	2050	6	AR559688	Sequence

#### ALIGNMENTS

RESULT 1	AF358860	AF358860	1593 bp	mRNA	linear	ROD 02-SEP-2001
LOCUS	Rattus norvegicus	histamine H4 receptor mRNA, complete cds.				
DEFINITION	Rattus norvegicus	histamine H4 receptor mRNA, complete cds.				
ACCESSION	AF358860					
VERSION	AF358860.1	GI:15420536				
KEYWORDS	Rattus norvegicus (Norway rat)					
SOURCE	Rattus norvegicus					
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.					
REFERENCE	1 (bases 1 to 1593)					
AUTHORS	Liu, C., Wilson, S., Kuei, C. and Lovenberg, T.W.					
TITLE	Comparison of human, mouse, rat, and guinea pig histamine H4 receptor suggests substantial species variation					
JOURNAL	Unpublished					
REFERENCE	2 (bases 1 to 1593)					
AUTHORS	Liu, C., Wilson, S., Kuei, C. and Lovenberg, T.W.					
TITLE	Direct Submision					
JOURNAL	Submitted (12-MAR-2001) Molecular Pharmacology, The R.W. Johnson Pharmaceutical Research Institute, 3210 Merryfield Row, San Diego, CA 92121, USA					
FEATURES	Location/Qualifiers					
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	/mol_type="mRNA"					
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ORIGIN
Alignment Scores:
Pred. No.: 1
Score: 1593
Percent Similarity: 99.74%
Best Local Similarity: 99.74%
Query Match: 99.46%
DB: 10
Gaps: 0
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QY 1 MetSerGluSerAanGlyThrAspValLeuProLeuThrAlaGlnValProLeuAlaPhe 20
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QY 21 LeuMetSerLeuLeuAlaPheAlaIleThrIleGlyAsnAlaValAlaLeuAlaPhe 40
DB 96 TTAATGTCCTGCTGCTTGTCTATACGATAGGCAATGCTGTGGTCAATTTAGCTTT 155
QY 41 ValAlaSerArgAanLeuArgHisArgSerAanTyrPhePheLeuAanLeuAlaIleSer 60
DB 156 GTAGCAGACAGAACCTTAGACATCGAAGTAATATTTTCTTAATTTGGCTATTCT 215
QY 61 AspPhePheValGlyValIleSerIleProLeuTyrIleProHisThrLeuPheAsnTyr 80
DB 216 GACTTCTTCGGGTGTCATCTCCATTCCTCTGACATCCCTCAGCTGTTAACTGG 275
QY 81 AsnProGlySerGlyIleCysMetPheThrIleThrAspTyrLeuLeuCysThrAla 100
DB 276 AATTTTGGAGTGAATCTGATGTTTGGCTCATTACTGACTATCTTTGTGCACAGCA 335
QY 101 SerValTyrSerIleValLeuIleSerTyrAspArgTyrGlnSerValSerAanAlaVal 120
DB 336 TCCGCTACAGTATTGCTCTCATAGTACCATCCAGTACCATCCAGTCTTCAAGCGCTGTG 395
QY 121 ArgTyrArgAlaGlnHisThrGlyIleLeuLeuValAlaGlnMetValAlaValTyr 140
DB 396 CGTTATAGACAGACAGCAGCTGGCATCTGGAATTTGTTGCTCAAAATGGTGGCTTGG 455
QY 141 IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTyrIleAsnSer 160
DB 456 ATACTGCTTCTTGGTCAATGGCCCAATGATCTGGCTTCGGATTTTGAAGAACAGC 515
QY 161 ThrAsnThrGluGlyCysGluProGlyPheValThrGluTyrIleLeuAlaIleThr 180
DB 516 ACCAACACAGAGAGTGGAGCTTGGCTTGTACTGAGTGGTACATCCCTCGCATTACA 575
QY 181 AlaPheLeuGluPheLeuLeuProValSerLeuValValTyrPheSerValGlnIleTyr 200
DB 576 GCATTTCTTGGAAATTCCTGCTCCCTGCTCTCTGTTGGTGTCTATTTCAAGTGTACATTTAC 635
QY 201 TrpSerLeuTyrIleAspGlySerLeuSerArgCysProSerHisAlaGlyPheIleAla 220
DB 636 TGGAGCTGTGGAAGCGTGGAGTCTCAGTAGTGGCTTACCCAGCTGAGTGTATTCGCT 695
QY 221 ThrSerSerArgGlyThrGlyHisSerArgArgThrGlyLeuAlaCysArgThrSerLeu 240
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ORIGIN

Alignment Scores:

Pred. No.: 1

Score: 1593

Percent Similarity: 99.74%

Best Local Similarity: 99.74%

Query Match: 99.46%

DB: 10

Gaps: 0

US-10-626-126-9 (1-391) x AF358860 (1-1593)

QY 1 MetSerGluSerAanGlyThrAspValLeuProLeuThrAlaGlnValProLeuAlaPhe 20

DB 36 ATGTCGAGTCTAACGGCAGCTGCTTGGCAGTCTGCTCAAGTCCCTCGCATTT 95

QY 21 LeuMetSerLeuLeuAlaPheAlaIleThrIleGlyAsnAlaValAlaLeuAlaPhe 40

DB 96 TTAATGTCCTGCTGCTTGTCTATACGATAGGCAATGCTGTGGTCAATTTAGCTTT 155

QY 41 ValAlaSerArgAanLeuArgHisArgSerAanTyrPhePheLeuAanLeuAlaIleSer 60

DB 156 GTAGCAGACAGAACCTTAGACATCGAAGTAATATTTTCTTAATTTGGCTATTCT 215

QY 61 AspPhePheValGlyValIleSerIleProLeuTyrIleProHisThrLeuPheAsnTyr 80

DB 216 GACTTCTTCGGGTGTCATCTCCATTCCTCTGACATCCCTCAGCTGTTAACTGG 275

QY 81 AsnProGlySerGlyIleCysMetPheThrIleThrAspTyrLeuLeuCysThrAla 100

DB 276 AATTTTGGAGTGAATCTGATGTTTGGCTCATTACTGACTATCTTTGTGCACAGCA 335

QY 101 SerValTyrSerIleValLeuIleSerTyrAspArgTyrGlnSerValSerAanAlaVal 120

DB 336 TCCGCTACAGTATTGCTCTCATAGTACCATCCAGTACCATCCAGTCTTCAAGCGCTGTG 395

QY 121 ArgTyrArgAlaGlnHisThrGlyIleLeuLeuValAlaGlnMetValAlaValTyr 140

DB 396 CGTTATAGACAGACAGCAGCTGGCATCTGGAATTTGTTGCTCAAAATGGTGGCTTGG 455

QY 141 IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTyrIleAsnSer 160

DB 456 ATACTGCTTCTTGGTCAATGGCCCAATGATCTGGCTTCGGATTTTGAAGAACAGC 515

QY 161 ThrAsnThrGluGlyCysGluProGlyPheValThrGluTyrIleLeuAlaIleThr 180

DB 516 ACCAACACAGAGAGTGGAGCTTGGCTTGTACTGAGTGGTACATCCCTCGCATTACA 575

QY 181 AlaPheLeuGluPheLeuLeuProValSerLeuValValTyrPheSerValGlnIleTyr 200

DB 576 GCATTTCTTGGAAATTCCTGCTCCCTGCTCTCTGTTGGTGTCTATTTCAAGTGTACATTTAC 635

QY 201 TrpSerLeuTyrIleAspGlySerLeuSerArgCysProSerHisAlaGlyPheIleAla 220

DB 636 TGGAGCTGTGGAAGCGTGGAGTCTCAGTAGTGGCTTACCCAGCTGAGTGTATTCGCT 695

QY 221 ThrSerSerArgGlyThrGlyHisSerArgArgThrGlyLeuAlaCysArgThrSerLeu 240

DB 696 ACCTCTTCCAGGGGCACTGGACACTCAGCAGAACTGGGTTGGCTTGTAGACAACTGCTT 755

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## ORIGIN

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Score: 1742.00 Matches: 332  
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Best Local Similarity: 84.91% Mismatches: 42  
Query Match: 85.18% Indels: 0  
DB: 10 Gaps: 0

US-10-626-126-9 (1-391) x AF358859 (1-1538)

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Qy 21 LeuMetSerLeuLeuAlaPheAlaIleThrIleGlyAenAlaValValIleLeuAlaPhe 40  
Db 121 TTAATGCTTCATTTGGCTTTGCTATATAGTAGGCAATGCTGTGGTTCATCTTAGCCCTT 180  
Qy 41 ValAlaAspArgAsnLeuAtgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60  
Db 181 GTGGTGACACACCTAGACATCGAAGTAATATTTTCTTAAATGGCTATTCT 240  
Qy 61 AspPheValGlyValIleSerIleProLeuTyrIleProHisThrLeuPheAsnTrp 80  
Db 241 GACTTCTCGTGGGTTGATTTCCATCTCTGTACATCCCTCAGCTGTGTTAACTGG 300  
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Db 301 AATTTTGGAGTGAAATCTGCATGTTTGGCTCATTAAGTACTGACTATCTTTTGTGACCGCA 360  
Qy 101 SerValTyrSerIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120  
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Qy 121 ArgTyrArgAlaGlnHisThrGlyIleLeuIleValAlaGlnMetValAlaValTrp 140  
Db 421 TCTTATAGGGCTCAACACACTGGCATCATGAAGATTTGTTGCTCAAAATGGTGGCTTGG 480  
Qy 141 IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTrpIleAsnSer 160  
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Qy 261 LeuLeuValSerLeuArgThrHisMetSerGlySerIleIleAlaPheValGlySer 280  
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Qy 301 ArgIleLeuAlaArgSerLeuAlaValLeuLeuSerAlaPheAlaIleCysTrpAlaPro 320  
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Qy 321 TyrCysLeuPheThrIleValLeuSerThrTyrArgArgGlyGluArgProIleSerIle 340  
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Qy 341 TrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerLeuIleAsnProPheLeuTyr 360  
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Qy 381 ProAlaProSerGlnThrGlnSerValSerSer 391  
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RESULT 3  
AC118386/c 236694 bp DNA linear HTG 15-NOV-2002  
LOCUS Rattus norvegicus clone CH230-397N16, \*\*\* SEQUENCING IN PROGRESS  
DEFINITION Rattus norvegicus (Norway rat)  
AC118386  
VERSION AC118386.4 GI:25013229  
KEYWORDS HTG; HTGS PHASE1; HTGS DRAFT; HTGS\_ENRICHED.  
SOURCE Rattus norvegicus (Norway rat)  
ORGANISM Rattus norvegicus  
REFERENCE 1 (bases 1 to 236694)  
AUTHORS Muzny D, Marie, Metzker M, Lee, Abramson S, Adams C, Alder J, Allen C, Allen H, Alsebrook S, Amin A, Anguiano D, Anyalebechi V, Aoyagi A, Ayodeji M, Baca E, Baden H, Baldwin D, Bandaranaike D, Barber M, Barnstead M, Benahmed F, Biswal K, Blair J, Blankenburg K, Blyth P, Brown M, Bryant N, Buhay C, Burch P, Burrell K, Calderon E, Cardenas V, Carter K, Cavazos I, Ceasar H, Center A, Chacko J, Chavez D, Chen G, Chen R, Chen Y, Chen Z, Chu J, Cleveland C, Cockrell R, Cox C, Coyte M, Cree A, D'Souza L, Devila M, Davis C, Davy-Carroll L, De Anda C, Dederich D, Delgado O, Denison S, Deramo C, Ding Y, Dinh H, Divya K, Draper H, Dugan-Rocha S, Dunn A, Durbin K, Duval B, Eaves K, Egan A, Escotto M, Eugene C, Evans C, Falls T, Fan G, Fernandez S, Finley M, Flagg N, Forbes L, Foster M, Foster P, Fraser C, Gabis A, Ganta R, Garcia A, Garner T, Garza M, Gebregorgis E, Geer K, Gill R, Grady M, Guerra W, Guevara W, Gunaratne P, Haaland W, Hamill C, Hamilton C, Hamilton K, Harvey Y, Havlak P, Hawes A, Henderson N, Hernandez J, Hernandez R, Hines S, Hladun S, Hodgson A, Hughes M, Hollins B, Howells S, Hulyk S, Hume J, Idlebird D, Jackson A, Jackson L, Jacob L, Jiang H, Johnson B, Johnson R, Jolivet A, Karpachy S, Kelly S, Khan Z, King L, Kovar C, Kowis C, Kraft C, Lebow H, Levan J, Lewis L, Li Z, Liu J, Liu J, Liu W, Liu Y, London P, Longacre S, Lopez J, Lorenzuehwa L, Loulseghe H, Lozano R, Lu X, Ma J, Maheshwari M, Mahindartine M, Mahmoud M, Malloy K, Mangum A, Mangum B, Mapus P, Martin K, Martin R, Martinez E, Mathewney S, McLeod M, McNeill T, Meenen E, Milosavljevic A, Miner G, Minja E, Montemayor J, Moore S, Morgan M, Morris K, Morris S, Munidasa M, Murphy M, Nair L, Nankervis C, Neal D, Newton N, Nguyen N, Norris S, Nwankwelu O, Okwunodu G, Olarnpunsagoon A, Pal S, Parks K, Pasternak S, Paul H, Perez A, Perez L, Pfannkuch C, Plummer F, Poindestier A, Popovic D, Primus E, Pu L, Puzo M, Quiroz J, Rachlin E, Reeves K, Regier M, Reigh R, Reilly B, Reilly M, Ren Y, Reuter M, Richards S, Riggs F, Rives C, Rodkey T, Rojas A, Rose M, Rose R, Ruiz S, Sanders W, Savery G, Scherer S, Scott G, Shatman S, Shen H, Shetty J, Shvartsbeyn A, Sisson I, Sitter C, Smajs D,



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Db 183453 ATTTGGTACAGATTGCTTTTGGCTACAGTGTTCATTCAATTCATTAACTCCCTTCTTA 183394
Qy 360 TyrProLeuCysHisArgArgPheGlnLysAlaPheTrpLysIleLeuCysValThrLys 379
Db 183393 TACGCTTTGTGCCACAGAGCTTTCAGAAAGCTTTCTGGAAGACTCTGTGTGACAAAG 183334
Qy 380 GlnProAlaProSerGlnThrGlnSerValSerSer 391
Db 183333 CAGCAGCACCTTCACAGACCAGTCAGTACTTCT 183298

RESULT 4
AY008280 1173 bp mRNA linear PRI 15-MAR-2004
LOCUS AY008280 Homo sapiens histamine receptor H4 (H4) mRNA, complete cds.
DEFINITION AY008280
ACCESSION AY008280.1 GI:15822540
VERSION AY008280.1
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1173)
Nguyen,T., Shapiro,D.A., George,S.R., Setola,V., Lee,D.K.,
Cheng,R., Rauser,L., Lee,S.P., Lynch,K.R., Roth,B.L. and
O'Dowd,B.P.
O'Dowd,B.P.
Discovery of a novel member of the histamine receptor family
Mol. Pharmacol. 59 (3), 427-433 (2001)
21106319
PUBMED 11179435
REFERENCE 2 (bases 1 to 1173)
Nguyen,T., George,S.R., Lee,D.K., Cheng,R., Lynch,K.R. and
O'Dowd,B.P.
O'Dowd,B.P.
Discovery of H4, a Novel Histamine Receptor
Unpublished
3 (bases 1 to 1173)
Nguyen,T., George,S.R., Lee,D.K., Cheng,R., Lynch,K.R. and
O'Dowd,B.P.
Direct Submission
TITLE Submitted (26-SEP-2000) Pharmacology, University of Toronto, 8
JOURNAL Taddle Creek Rd., Rm. 4353, Toronto, Ont M5S 1A8, Canada
AUTHORS Location/Qualifiers
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Alignment Scores:
Pred. No.: 2,09e-107 Length: 1173
Score: 1405.50 Matches: 271
Percent Similarity: 79.59% Conservative: 41

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Best Local Similarity: 69.13% Mismatches: 77
Query Match: 68.73% Indels: 3
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RESULT 5
LOCUS AR142850
DEFINITION Sequence 1 from patent US 6204017.
ACCESSION AR142850
VERSION AR142850.1 GI:15104136
KEYWORDS
SOURCE
ORGANISM
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REFERENCE 1 (bases 1 to 1173)
AUTHORS Behan,J.X., Hedrick,J.A., Laz,T.M., Monsma,F.J., Morse,K.L.,
Unland,S.P. and Wang,S.
TITLE Polynucleotide encoding a histamine receptor
JOURNAL Patent: US 6204017-A 1 20-MAR-2001;
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ORIGIN
Alignment Scores:
Pred. No.: 3,06e-107 Length: 1173
Score: 1403.50 Matches: 271
Percent Similarity: 79.34% Conservative: 40
Best Local Similarity: 69.13% Mismatches: 78
Query Match: 68.63% Indels: 3
DB: 6 Gaps: 2

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DEFINITION Sequence 1 from patent US 6613533.
ACCESSION AR391860
VERSION AR391860.1 GI:40115588
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AUTHORS Behan,J.X., Hedrick,J.A., Laz,T.M., Monsma,F.J., Morse,K.L.,
Unland,S.P. and Wang,S.
TITLE Histamine receptor
JOURNAL Patent: US 6613533-A 1 02-SEP-2003;
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Location/Qualifiers
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ORIGIN
Alignment Scores:

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Pred. No.: 3,06e-107 Length: 1173
Score: 1403.50 Matches: 271
Percent Similarity: 79.34% Conservative: 40
Best Local Similarity: 69.13% Mismatches: 78
Query Match: 68.63% Indels: 3
DB: 6 Gaps: 2

US-10-626-126-9 (1-391) x AK391860 (1-1173)

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ACCESSION AX109119
VERSION AX109119.1 GI:13924093
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SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Behan, J. X., Hedrick, J. A., Laz, T. M., Monema, P. J., Morse, K. L.,
Umland, S. and Wang, S.
TITLE Histamine receptor
JOURNAL Patent: WO 0125432-A 1 12-APR-2001;
SCHERING CORPORATION (US)
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US-10-626-126-9 (1-391) x AX109119 (1-1173)

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VERSION AX139113.1 GI:14274791  
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SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
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REFERENCE  
AUTHORS Peter.B. and O'Reilly.M.A.  
TITLE G-protein coupled receptor-like polypeptide  
JOURNAL Patent: EP 1096009-A 1 02-MAY-2001;  
Pfizer Limited (GB) ; PFIZER INC. (US)

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## ORIGIN

Alignment Scores:  
Pred. No.: 3,06e-107 Length: 1173  
Score: 1403.50 Matches: 271  
Percent Similarity: 79.34% Conservative: 40  
Best Local Similarity: 69.13% Mismatches: 78  
Query Match: 68.63% Indels: 3  
DB: 6 Gaps: 2

US-10-626-126-9 (1-391) x AX139113 (1-1173)

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Qy 241 ProGlyLeuLysGluProAlaAlaSerLeuHisSerLeuSerProArgGlyLysSerSer 260
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LOCUS
DEFINITION
ACCESSION AX301763
VERSION AX301763.1 GI:17382844
KEYWORDS
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ORGANISM Homo sapiens (human)
REFERENCE
AUTHORS Jones, P.G., Blatcher, M., Wu, S. and Pausch, M.H.
TITLE Human histamine h 4? receptor
JOURNAL Patent: WO 0185786-A 1 15-NOV-2001;
American Home Products Corporation (US)
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Query Match: 68.63% Indels: 3
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Qy 381 ProAlaProSerGln---ThrGlnSerValSerSer 391
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LOCUS
DEFINITION Novel polypeptide.
ACCESSION BD015847
VERSION BD015847.1 GI:22556984
KEYWORDS JP 2001211889-A/1.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

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DEFINITION Novel polypeptide.
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KEYWORDS JP 2001211889-A/1.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

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Best Local Similarity: 69.13% Mismatches: 78
Query Match: 68.63% Indels: 3
DB: 9 Gaps: 2
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VERSION  
KEYWORDS  
SOURCE Homo sapiens (human)  
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 1173)  
AUTHORS Zhu,Y., Michalovich,D., Wu,H.-L., Tan,K.B., Dytko,G.M.,  
Mannan,I.J., Boyce,R., Alston,J., Tierney,L.A., Li,X.,  
Herrity,N.C., Vawter,L., Sarau,H.M., Ames,R.S., Davenport,C.M.,  
Hieble,P., Wilson,S., Bergsma,D.J. and Fitzgerald,L.R.  
Cloning, expression, and pharmacological characterization of a  
novel human histamine receptor  
Mol. Pharmacol. 59 (3), 434-441 (2001)  
JOURNAL MEDLINE 21106320  
PUBMED 11179436  
REFERENCE 2 (bases 1 to 1173)  
AUTHORS Zhu,Y., Michalovich,D. and Fitzgerald,L.R.  
Direct Submission  
TITLE Submitted (30-NOV-2000) GlaxoSmithKline, 709 Swedeland Rd., PO Box  
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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AUTHORS Morse, K.L., Behan, J., Laz, T.M., West, R.E. Jr., Greenfeder, S.A.,
Athos, J.C., Umland, S., Wan, Y., Hipkin, R.W., Gonsiorek, W., Shin, N.,
Gustafson, E.L., Qiao, X., Wang, S., Hedrick, J.A., Greene, J., Bayne, M.,
and Monsma, F.J. Jr.
TITLE Cloning and characterization of a novel human histamine receptor
JOURNAL J. Pharmacol. Exp. Ther. 296 (3), 1058-1066 (2001)
MEDLINE 21104636
PUBMED 11181941
REFERENCE 2 (bases 1 to 1173)
AUTHORS Monsma, F.J. Jr., Wang, S., Behan, J., Laz, T.M., Greene, J. and
Bayne, M.
TITLE Direct Submission
JOURNAL Submitted (15-DEC-2000) Human Genomics Research, Schering-Plough
Research Institute, 2015 Galloping Hill Rd., Kenilworth, NJ 07033,
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LOCUS HSA298292 1173 bp mRNA linear PRI 12-JAN-2002
DEFINITION Homo sapiens mRNA for histamine receptor H4 (HRH4 gene).
ACCESSION AJ298292
VERSION AJ298292.1 GI:18152452
KEYWORDS histamine receptor H4; HRH4 gene.
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS O'Reilly, M.A.
TITLE Identification of a histamine H4 receptor on human eosinophils -
JOURNAL Role in eosinophil chemotaxis
AUTHORS Unpublished
TITLE 2 (bases 1 to 1173)
AUTHORS O'Reilly, M.A.
JOURNAL Direct Submission
TITLE Submitted (11-JAN-2001) O'Reilly M.A., Discovery Biology, Pfizer
JOURNAL Ltd, Ramsgate Road, Sandwich, Kent, CT13 9NJ, UNITED KINGDOM
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GSECPGFSEWYILAITSFLEFVIVLVAIFNNIYMSLWKRDHLSCQHPGLTA
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GSPSQSDVALHOREHVELLRARLAKSLAILLGVFVAVCWAPYSLFTIIVLSFVSATG
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US-10-626-126-9 (1-391) x HSA298292 (1-1173)
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Db 61 TTTATGTCCTTAGTACCTTTCTAATAAGTAGGAAATGCTTTGGTCAATTTAGCTTTT 120
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Qy 181 AlaPheLeuGluPheLeuLeuProValSerLeuValValTyrPheSerValGlnIleTyr 200
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Qy 201 TrpSerLeuTrpLysArgGlySerLeuSerArgCysProSerHisAlaGlyPheIleAla 220
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Db 715 TCTGCATCGACAGAAGTTCCTGCATCTCTTTCATTTCAGAGAGACAGAGGAGAAAGAGTAGT 774
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Qy 321 TyrCysLeuPheThrIleValLeuSerThrTyrArgArgGlyGluArgProLysSerIle 340
Db 955 TATTCTCTGTTCACAATTGCTCTTTCATTTTATTTCTCTCAGCAACAGGTCCTAAATCAGTT 1014
Qy 341 TrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerLeuIleAsnProPheLeuTyr 360
Db 1015 TGGTATAGAAATTCATTTTGGCTTCAGTGGTTCAATTCCTTTGTCAATCTCTTTTGTAT 1074
Qy 361 ProLeuCysHisArgArgPheGlnLysAlaPheTrpLysIleLeuCysValThrLysGln 380
Db 1075 CCATTGTGTCAACAGCGCTTCAAAGGCTTTCTTGAATAATATTTGTATAAAAAGCAA 1134
Qy 381 ProAlaProSerGln---ThrGlnSerValSerSer 391
Db 1135 CCTCTACCATCACAAACACAGTCGGTCAGTATCTTCT 1170
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: August 5, 2005, 12:17:55 ; Search time 573 Seconds

(without alignments)  
4039.474 Million cell updates/sec

Title:

US-10-626-126-9

Perfect score: 2045

Sequence: 1 MSESNGTDVLPVTAQVPLAF.....WKILCVTKQAPASQTSVSS 391

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi  
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12: Geneseqn2004as:\*  
13: Geneseqn2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	1742	85.2	1176	6	Aai70981 Mouse his
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4	1403.5	68.6	1170	9	Aad55126 Human H4
5	1403.5	68.6	1173	3	Aaa46023 Human G p

6	1403.5	68.6	1173	3	AAD01124	Aad01124 Human orp
7	1403.5	68.6	1173	4	AAF83203	Aaf83203 Human GPC
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17	1403.5	68.6	1173	12	ADG86374	Adg86374 Human end
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36	693	33.9	1335	4	AAH44573	Aah44573 Human mus
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#### ALIGNMENTS

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ID AAI70982 standard; cdna; 1176 BP.  
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AC AAI70982;  
XX  
DT 18-MAR-2002 (first entry)  
XX  
DE Rat histamine H4 receptor cdna.  
XX  
KW Histamine H4 receptor; rat; antiasthmatic; antiallergenic;  
KW antiinflammatory; cardiant; circulatory; antidiabetic; laxative;  
KW diagnosis; gene therapy; ss.  
XX  
OS Rattus rattus.  
XX  
FN WO200192485-A1.  
XX  
PD 06-DEC-2001.  
XX  
PF 22-FEB-2001; 2001WO-US005914.  
XX  
PR 31-MAY-2000; 2000US-0208260P.  
XX  
(ORTH ) ORTHO-MCNEIL PHARM INC.  
XX  
PI Lovenberg T, Liu C;  
XX  
DR WPI; 2002-114339/15.

DR P-P8DB; AAM50566.  
 XX New mammalian histamine H4 receptor proteins and polynucleotides encoding  
 PT the proteins, useful in gene therapy for treating diseases where it is  
 PT beneficial to elevate mammalian histamine H4 receptor activity.  
 XX  
 XX  
 PS Claim 4; Fig 5C; 92pp; English.  
 CC  
 CC The present sequence is that of a cDNA clone encoding a rat histamine  
 CC receptor of the H4 subtype. The cDNA was isolated from a rat spleen cDNA  
 CC library. It shows 72.5% homology to the human H4 receptor coding region.  
 CC The invention provides mammalian (human, mouse, rat and guinea pig)  
 CC histamine H4 receptor nucleic acid molecules (see AAI70980-83) and  
 CC polypeptides (see AAM50564-67). The nucleic acids have been expressed in  
 CC recombinant host cells that produce active recombinant protein. The  
 CC pharmacology of known histamine ligands is demonstrated. Mammalian  
 CC histamine H4 receptor may be used in gene therapy for the treatment of  
 CC diseases where it is beneficial to elevate mammalian histamine H4  
 CC receptor activity. Recombinant protein is useful for identifying  
 CC modulators of the mammalian histamine H4 receptor. Such modulators may be  
 CC useful for diagnosing, treating or preventing asthma, allergy,  
 CC inflammation, cardiovascular and cerebrovascular disorders, non-insulin  
 CC dependent diabetes mellitus, hyperglycemia, constipation, arrhythmia,  
 CC disorders of the neuroendocrine system, stress and spasticity  
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US-10-626-126-9 (1-391) x AAI70982 (1-1176)

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 QY 81 AsnProGlySerGlyIleCysMetPheThrLeuIleThrAspTyrLeuLeuCysThrAla 100  
 DB 241 AATTTTGGAGTGAATCTGCATGTTTGGCTCATTTACTGACTATCTTTTGGCAGCA 300  
 QY 101 SerValTyrSerIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120  
 DB 301 TCCGCTACAGATATTGCTCTCATTTAGCTACGATCGATACAGTCAGTCTTCAAAACGCTGTG 360  
 QY 121 ArgTyrArgAlaGlnHisThrGlyIleLeuValIleValAlaGlnMetValAlaValTyr 140  
 DB 361 CGTTATAGACACAGACACACTGCACTCCCTGAAATTTGTTGCTCAAAATGGTGGCTGTTGG 420  
 QY 141 IleLeuAlaPheLeuValAsnGlyPrometIleLeuAlaSerAspSerTyrIleAsnSer 160  
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 QY 281 PheCysArgSerGluSerProValLeuHisGlnArgGluHisValGluLeuLeuArgGly 300  
 DB 841 TTCTCCGATCAGAAAGCCAGTGTCTTACCAGAGAGACGCTGGAGCTTCTCAGAGGC 900  
 QY 301 ArgLysLeuAlaArgSerLeuAlaValLeuLeuSerAlaPheAlaIleCysTrpAlaPro 320  
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 DB 1081 CTTTGTGCCACAGACGTTTCCAGAGGCTTCTGGAAGATACTCTGTGTGCAAGCA 1140  
 QY 381 ProAlaProSerGlnThrGlnSerValSerSer 391  
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 DT 18-MAR-2002 (first entry)  
 DE Mouse histamine H4 receptor cDNA.  
 KW Histamine H4 receptor; mouse; antiasthmatic; antiallergenic;  
 KW antiinflammatory; cardiant; circulatory; antidiabetic; laxative;  
 KW diagnosis; gene therapy; ss.  
 OS Mus musculus.  
 XX WO200192485-A1.  
 PN 06-DEC-2001.  
 PD 22-FEB-2001; 2001WO-US005914.  
 PF 31-MAY-2000; 2000US-0208260P.  
 PR (ORTH ) ORTHO-MCNEIL PHARM INC.  
 PA Lovenberg T, Liu C;  
 PI WPI; 2002-114339/15.  
 DR

DR P-PSDB; AAM50565.

XX New mammalian histamine H4 receptor proteins and polynucleotides encoding

PT the proteins, useful in gene therapy for treating diseases where it is

PT beneficial to elevate mammalian histamine H4 receptor activity.

XX Claim 4; Fig 5A; 92pp; English.

XX The present sequence is that of a cDNA clone encoding a murine histamine

CC receptor of the H4 subtype. The cDNA was isolated from a mouse spleen

CC cDNA library. It shows 72.8% homology to the human H4 receptor coding

CC region. The invention provides mammalian (human, mouse, rat and guinea

CC pig) histamine H4 receptor nucleic acid molecules (see AAI70980-83) and

CC polypeptides (see AAM50564-67). The nucleic acids have been expressed in

CC recombinant host cells that produce active recombinant protein. The

CC pharmacology of known histamine ligands is demonstrated. Mammalian

CC histamine H4 receptor may be used in gene therapy for the treatment of

CC diseases where it is beneficial to elevate mammalian histamine H4

CC receptor activity. Recombinant protein is useful for identifying

CC modulators of the mammalian histamine H4 receptor. Such modulators may be

CC useful for diagnosing, treating or preventing asthma, allergy,

CC inflammation, cardiovascular and cerebrovascular disorders, non-insulin

CC dependent diabetes mellitus, hyperglycemia, constipation, arrhythmia,

CC disorders of the neuroendocrine system, stress and spasticity

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SQ Sequence 1176 BP; 263 A; 281 C; 269 G; 363 T; 0 U; 0 Other;

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DB:	6	Gaps:	0

US-10-626-126-9 (1-391) x AAI70981 (1-1176)

QY 1 MetSerGluSerAsnGlyThrAspValLeuProLeuThrAlaGlnValProLeuAlaPhe 20

DB 1 ATGTGGAGTCTAACAGTACTGTCATCTGCCACCAGCTGCTCAGGTCCCTTGGCATTT 60

QY 21 LeuMetSerLeuLeuAlaPheAlaIleThrIleGlyAsnAlaValValIleLeuAlaPhe 40

DB 61 TTAATGTCTTCATTTGCCCTTTGGTATTAAGTGGCAATGCTGTGTCATCTTAGCCTTT 120

QY 41 ValAlaAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60

DB 121 GTGGTGGACAGAAACCTTAGACATCGAAGTAATATTTTCTTAATTTGGCTATTCTT 180

QY 61 AspPhePheValGlyValIleSerIleProLeuTyrIleProHisThrLeuPheAsnTrp 80

DB 181 GACTTCTCTGTGGTGTGATTTCCATTCCTCTGTACATCCCTCAGCGTGTGTTAACTGG 240

QY 81 AsnProGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeuLeuCysThrAla 100

DB 241 AATTTGGAGAGTGGATCTGCATGTTTGGCTCATTTACTGACTATCTTTTGTGACCGCA 300

QY 101 SerValTyrSerIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120

DB 301 TCTGTCTACAAATATGTCCTCATAGCTACATGATCAGTACAGTTCCTCAATGCTGTG 360

QY 121 ArgTyrArgAlaGlnHisThrGlyIleLeuLeuIleValAlaGlnMetValAlaValTrp 140

DB 361 TCTTATAGGCTCAACACACTGTCATCATGAGATTGTTCTCAATGGTGGCTGTTGG 420

QY 141 IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTrpLeuAsnSer 160

DB 421 ATACTGGCTTTCTTGGTAAATGGCCCGCATGATTTCTGGCTTTTCTGAGTAAAGACAGC 480

QY 161 ThrAsnThrGluGluCysGluProGlyPheValThrGluTrpTyrIleLeuAlaIleThr 180

DB 481 ACGAACACAAAGGACTGTGAGCTTGGCTTTGTTTACAGAGTGGTACATCTCACCATTACA 540

QY 181 AlaPheLeuGluPheLeuLeuProValSerLeuValValTyrPheSerValGlnIleTyr 200

DB 541 ATGCTCTTTGGAAATTCCTGCTTCTGTCATCTCTGTCCTTATTTCAATGTACAGATTAC 600

QY 201 TrpSerLeuTrpLysArgGlySerLeuSerArgCysProSerHisAlaGlyPheIleAla 220

DB 601 TGGAGCTGTGGAAGCTAGGGCTCTCAGTAGTGCCCTAGCCATGCTGGATTCTCACT 660

QY 221 ThrSerSerArgGlyThrGlyHisSerArgThrGlyLeuAlaCysArgThrSerLeu 240

DB 661 ACTCTTTCAGTGTCTTCAGGACACTTACACAGAGCTGGGTGGCTTCAGGACAAGTAAT 720

QY 241 ProGlyLeuLysGluProAlaAlaSerLeuHisSerGluSerProArgGlyLysSerSer 260

DB 721 CTGGGATTCAGGAATCAGCTGCATCTCTGCTACTCAGAAAGTCTTCGAAAGAAAGACAGC 780

QY 261 LeuLeuValSerLeuArgThrHisMetSerGlySerIleIleAlaPheLysValGlySer 280

DB 781 ATCCTGTGTCTTAAAGGACTCACAACAGCAGTATCACTGCTTCAAGTGGGTTC 840

QY 281 PheCysArgSerGluSerProValLeuHisGlnArgGluHisValGluLeuLeuArgGly 300

DB 841 TTCTGGCGATCGAAAGTGCAGCGCTTCGCCAAAGGGAGTACGCAGAGCTTCTCAGAGGC 900

QY 301 ArgLysLeuAlaArgSerLeuAlaValLeuLeuSerAlaPheAlaIleCysTrpAlaPro 320

DB 901 AGGAGCTAGCCAGGTCACTGGCCATCTTCTGAGCGCTTTTGCCATTTGCTGGGTCCA 960

QY 321 TyrCysLeuPheThrIleValLeuSerThrTyrArgArgGlyGluArgProLysSerIle 340

DB 961 TACTGTCTGTTCACAAATGTGCTTTCACTTACCCAGAACGAGCCCAATCGGTG 1020

QY 341 TrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerLeuIleAsnProPheLeuTyr 360

DB 1021 TGGTACAGCATTCCTTCTGGCTGCAATGTTCAATTCGTTGTTAATCCCTTCTGTAC 1080

QY 361 ProLeuCysHisArgArgPheGlnLysAlaPheTrpLysIleLeuCysValThrLysGln 380

DB 1081 CCTTTGTGTACAGCGCTTTCAGAAAGGCTTTCTGGAAGATACTTTGTGTGACAAAGCAA 1140

QY 381 ProAlaProSerGlnThrGlnSerValSerSer 391

DB 1141 CCAGCCTGTCCAGAACCAACGATCAGTATCTTCT 1173

RESULT 3

AD030257

ID AD030257 standard; cDNA; 1538 BP.

XX AD030257;

XX 29-JUL-2004 (first entry)

DE Mouse GPCR HRH4 polynucleotide, SEQ ID NO:1360.

XX G protein-coupled receptor; GPCR; drug screening; diagnosis;

KW transgenic mouse; neurological disorder; adrenal gland disorder;

KW colon disorder; intestinal disorder; cardiovascular disorder;

KW muscular disorder; blood disorder; immune disorder; bone disorder;

KW joint disorder; metabolic disorder; nutritive disorder; cancer;

KW kidney disorder; liver disorder; lung disorder; breast disorder;

KW ovary disorder; uterus disorder; prostate disorder; testis disorder;

KW skin disorder; stomach disorder; pancreas disorder; spleen disorder;

KW thymus disorder; thyroid disorder; antiparkinsonian; antimanic;

KW cytostatic; antiinflammatory; vasotropic; antianginal; antiarrhythmic;

KW CNS; central nervous system; respiratory; antidiarrhoeic; antidiabetic;

KW virucide; hepatotropic; antibacterial; antianemic; antiseborrhoeic;

KW dermatological; antilucer; antithyroid; antiallergic; anorectic;

KW immunosuppressive; nephrotropic; gene therapy; GPCR modulator; mouse;

KW murine; gene; ss.

XX Mus musculus.

OS

XX WO2004040000-A2.

PN



XX 13-MAY-2004.  
 PD 09-SEP-2003; 2003WO-US028226.  
 PF 09-SEP-2002; 2002US-0409303P.  
 PR 09-APR-2003; 2003US-0461329P.  
 XX (PRIM-) PRIMAL INC.  
 PA  
 XX Gaitanaris GA, Bergmann JE, Gragerov A, Hohmann J, Li F;  
 PI Madisen L, McIlwain KL, Pavlova MN, Vassiliadis D, Zeng H;  
 XX WPI: 2004-390329/36.  
 DR P-PSDB; ADO29497.  
 XX Novel mammalian G protein coupled receptors, useful for identifying  
 PT compounds that modulates diagnosing and treating disease condition  
 PT associated with GPCR dysfunction e.g. autoimmune diseases, angina  
 PT pectoris, Parkinson's disease.  
 XX Claim 151; SEQ ID NO 1360; 542pp; English.  
 PS The invention relates to human and mouse G protein-coupled receptors  
 CC (GPCRs) and nucleic acids encoding them. The invention also relates to  
 CC sequences at least 90% identical to the GPCR proteins and nucleic acids  
 CC of the invention; methods of treating, preventing or diagnosing diseases  
 CC associated with GPCRs of the invention; methods of screening for  
 CC compounds useful in the treatment of GPCR-related diseases; a transgenic  
 CC mouse comprising a GPCR gene of the invention; a mouse comprising a  
 CC mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived  
 CC from the transgenic mice; kits comprising several mice, each of which has  
 CC a mutation in a different GPCR gene of the invention; and kits comprising  
 CC probes which hybridize to GPCR polynucleotides of the invention. The  
 CC invention further discloses variants of the GPCR polypeptides and vectors  
 CC comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may  
 CC be used in the diagnosis, treatment or prevention of a wide variety of  
 CC diseases including neurological disorders (e.g., Alzheimer's disease,  
 CC depression, diabetic neuropathy, Parkinson's disease or schizophrenia);  
 CC disorders of the adrenal gland; disorders of the colon or intestine  
 CC (e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel  
 CC syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or  
 CC myocardial infarction); muscular disorders; blood disorders (e.g.,  
 CC anaemia or leukaemia); immune disorders (e.g., autoimmune disorders or  
 CC AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid  
 CC arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g.,  
 CC obesity, enzyme deficiency-related diseases or vitamin deficiency-related  
 CC diseases); and disorders of the kidney, liver, lung, breast, ovary,  
 CC uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and  
 CC thyroid (e.g., cancers). The present sequence represents a GPCR-encoding  
 CC nucleic acid of the invention. Note: The full sequence data for this  
 CC patent did not form part of the printed specification; those sequences  
 CC not shown were obtained in electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences.  
 XX  
 SQ Sequence 1538 BP; 357 A; 362 C; 340 G; 479 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.: 1.13e-150 Length: 1538  
 Score: 1742.00 Matches: 332  
 Percent Similarity: 89.26% Conservative: 17  
 Best Local Similarity: 84.91% Mismatches: 42  
 Query Match: 85.18% Indels: 0  
 DB: 12 Gaps: 0

US-10-626-126-9 (1-391) x ADO30257 (1-1538)

QY 1 MetSerGluSerAsnGlyThrAspValLeuProLeuThrAlaGlnValProLeuAlaPhe 20  
 DB 61 ARGTCGGAGCTAACAGTACTGGCATCTTGGCCACACAGCTGCTCAGTCCCTTGGCATTT 120  
 QY 21 LeuMetSerLeuLeuAlaPheAlaIleThrIleGlyAsnAlaValValIleLeuAlaPhe 40

DB 121 TTAATGCTCTCATTTGGCCCTTTGCTATATAATGGTAGCAATGCTGGTGCATCTTAGCCCTTT 180  
 QY 41 ValAlaAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60  
 DB 181 GTGGTGGACAGAAACCTTAGACATCGAAGTAGTAATATTTTTTTCTTAATTTGGCTATTCT 240  
 QY 61 AspPhePheValGlyValIleSerIleProLeuTyrIleProHisThrLeuPheAsnTyr 80  
 DB 241 GACTTCCTCGTGGGTTTGATTTCCATTCTCTGTACATCCCTCAGCTGTTGTTTAACTGG 300  
 QY 81 AsnProGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeuLeuCysThrAla 100  
 DB 301 AATTTTGGAGTGGAAATCTGCATGTTTGGCTCATTACTGACTATCTTTTGTGCACCGCA 360  
 QY 101 SerValTyrSerIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120  
 DB 361 TCTGTCTACAATATTTGCTCTCATTTAGCTACGATCGATACCACTGCTTCAATCTGTG 420  
 QY 121 ArgTyrArgAlaGlnHisThrGlyIleLeuIleValAlaGlnMetValAlaValTyr 140  
 DB 421 TCTTATAGGCTCAACACACTGGCATCATGAAGATTGTTGCTCAATGGTGGCTGTTGG 480  
 QY 141 IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTrpIleAsnSer 160  
 DB 481 ATACTGGCTTTCTTGGTAAATGGCCGATGATTTCTGGCTTCAGATTCTTTGGAAGAACAG 540  
 QY 161 ThrAsnThrGluGluCysGluProGlyPheValThrGluTyrTyrIleLeuAlaIleThr 180  
 DB 541 ACGAAACACAAAGGACTGTGAGCTGGCTTGTGTACAGAGTGGTACATCTCCACCATTA 600  
 QY 181 AlaPheLeuGluPheLeuProValSerLeuValValTyrPheSerValGlnIleTyr 200  
 DB 601 ATGCTCTTGGAAATCTCTGCTCTCTGTCATCTCTGGCTTATTTCAATGTACAGATTAC 660  
 QY 201 TrpSerLeuTrpLysArgGlySerLeuSerArgCysProSerHisAlaGlyPheIleAla 220  
 DB 661 TGGAGCCTGTGGAAGCGTAGGCTCTCAGTAGTGGCTAGCCCTAGCCATGCTGGATTCTCC 720  
 QY 221 ThrSerSerArgGlyThrGlyHisSerArgThrGlyLeuAlaCysArgThrSerLeu 240  
 DB 721 ACCTCTCCAGTGGCTTTCAGACACTTACACAGAGCTGGGTGGCTTGCAGGACCAAGTAA 780  
 QY 241 ProGlyLeuLysGluProAlaAlaSerLeuHisSerGluSerProArgGlyLysSerSer 260  
 DB 781 CTGTGATTTGAAGGATCAGTGCATCTGCTACTCAGAAAGTCTCGAAGAAAGAGCAGC 840  
 QY 261 LeuLeuValSerLeuArgThrHisMetSerGlySerIleIleAlaPheLysValGlySer 280  
 DB 841 ATCTCTGGTGTCTTAAGGACTCACATGAACAGCAGTATCATCTTCAAGTGGGTTC 900  
 QY 281 PheCysArgSerGluSerProValLeuHisGlnArgGluHisValGluLeuLeuArgGly 300  
 DB 901 TTCTGGCATCGAAAGTGCAGCGCTTCGCCAAAGGGAGTAGCGCAGAGCTTCTCAGAGGC 960  
 QY 301 ArgLysLeuAlaArgSerLeuAlaValLeuLeuSerAlaPheAlaIleCysTrpAlaPro 320  
 DB 961 AGAAGCTAGCCAGGTCACTGGCCATCTTTCAGAGCGCTTTTGCCATTTGCTGGGCTCA 1020  
 QY 321 TyrCysLeuPheThrIleValLeuSerThrTyrArgArgGlyGluArgProLysSerIle 340  
 DB 1021 TACTGTGTTTCACAATTTGCTCTTTCACTTACCACGAGAACGCGCCCAATTCGGTG 1080  
 QY 341 TrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerLeuIleAsnProPheLeuTyr 360  
 DB 1081 TGGTACAGCATTTGCTTGGCTGCAATGGTTTCAATTCGTTTGTAAATCCCTTTCTGTAC 1140  
 QY 361 ProLeuCysHisArgPheGlnLysAlaPheTrpLysIleLeuCysValThrLysGln 380  
 DB 1141 CTTTTGTGTACAGCGGTTTCCAGAGGCTTCTCGAAGATACTTTGTGTGACAAAGCAA 1200  
 QY 381 ProAlaProSerGlnThrGlnSerValSerSer 391  
 DB 1201 CCAGCGCTGTCAAGAACCAAGTCAGTATCTTCT 1233

## RESULT 4

AAD55126

ID AAD55126 standard; DNA; 1170 BP.

XX AC AAD55126;

XX DT 07-AUG-2003 (first entry)

XX DE Human H4 receptor wild-type DNA #2.

XX KW Human; H4; histamine receptor; inflammatory bowel disease; psoriasis;

XX KW atopic dermatitis; stroke; myocardial infarction; migraine; allergy;

XX KW chronic obstructive pulmonary disease; COPD; cerebroprotective; therapy;

XX KW rheumatoid arthritis; multiple sclerosis; inflammation; neuroprotective;

XX KW asthma; receptor; gene; ds.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT CDS 1..1170

XX FT /\*tag= a

XX FT /product= "Human H4 protein"

XX FT /note= "CDS does not include stop codon"

XX FT /partial

XX PN W02003020907-A2.

XX PD 13-MAR-2003.

XX PF 30-AUG-2002; 2002WO-US027891.

XX PR 31-AUG-2001; 2001US-0316762P.

XX PR 13-NOV-2001; 2001US-0332697P.

XX XX (MERI ) MERCK &amp; CO INC. -

XX PI Gallagher MJ, Yates SL;

XX DR WPI; 2003-290186/28.

XX DR P-PSDB; AAE36417.

XX PT Novel splice variants of human H4 histamine receptor, H4b and H4c, useful

XX PT for identifying agonists or antagonists of the receptor which are useful

XX PT for treating multiple sclerosis, asthma, allergy, psoriasis and stroke.

XX PS Disclosure; Page 56-58; 31pp; English.

XX CC The invention relates to splice variants of human H4 histamine receptor,

XX CC H4b and H4c. The invention is useful for identifying an agonist,

XX CC antagonist or inverse agonist of a mammalian histamine receptor. The

XX CC agonist, antagonist or inverse agonist of H4b and H4c is useful for

XX CC treating inflammation, asthma, allergy, atopic dermatitis, stroke,

XX CC myocardial infarction, migraine, chronic obstructive pulmonary disease

XX CC (COPD), rheumatoid arthritis, multiple sclerosis, inflammatory bowel

XX CC disease, or psoriasis. The present sequence is human H4 receptor DNA

XX SQ Sequence 1170 BP; 292 A; 245 C; 231 G; 402 T; 0 U; 0 Other;

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21 LeuMetSerLeuLeuAlaPheAlaIleThrIleGlyAsnAlaValValIleLeuAlaPhe 40  
 61 TTTATGTCCTTAGTCTTTTGTCTAATAATGCTAGGAAATGCTTTGGTCACTTTTGTCTTTT 120  
 41 ValAlaAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuLeuAlaIleSer 60  
 121 GTGGTGACAAACCTTAGACATCGAAGTAGTATTTTTTTTCTTAACCTGGCACTCTCT 180  
 61 AspPhePheValGlyValIleSerIleProLeuTyrIleProHisThrLeuPheAsnTyr 80  
 181 GACTCTTTGGTGGTGTGATCTCCATCTCTTTGATACATCCCTCACAGCTGTTTGAATGG 240  
 81 AsnProGlySerGlyIleCysMetPheThrLeuLeuIleThrAspTyrLeuLeuCysThrAla 100  
 241 GATTTTGGAAAGGAAATCTGTGATTTTGGCTCACTACTGACTATCTGTTATGTACAGCA 300  
 101 SerValTyrSerIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120  
 301 TCTGTATATAACATTTGCTCTCATCAGCTATGATCGATACCTGTGAGTCTCAATAGCTGTG 360  
 121 ArgTyrArgAlaGlnHisThrGlyIleLeuLeuIleValAlaGlnMetValAlaValTyr 140  
 361 TCTTATAGAACTCAACATACCTGGGCTTGAAGATTGTTACTCTGATGGTGGCGTTTGG 420  
 141 IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTyrLeuAsnSer 160  
 421 GTGCTGGCTTCTTAGTGAATGGGCCAATGATTTCTAGTTTTCAGAGTCTTGGAAAGGATGAA 480  
 161 ThrAsnThrGluGluCysGluProGlyPheValThrGluTyrIleLeuAlaIleThr 180  
 481 GGTAGT-----GAATGTGAACCTGGATTTTTTTCGGAATGGTACATCTTGGCATCACA 534  
 181 AlaPheLeuGluPheLeuProValSerLeuValValTyrPheSerValGlnIleTyr 200  
 535 TCATTCTTGGAAATTCGTGATCCAGTCATCTTAGTCCTTATTTCAACATGAATATTAT 594  
 201 TrpSerLeuTrpLysArgGlySerLeuSerArgCysProSerHisAlaGlyPheIleAla 220  
 595 TGGAGCTGTGGAAAGCGTGATCATCTCAGTAGGTGCAAGCCATCTCTGGAGTCTGACTGCT 654  
 221 ThrSerSerArgGlyThrGlyHisSerArgThrGlyLeuAlaCysArgThrSerLeu 240  
 655 GTCTCTTCAACATCTGTGGACACTCATTCAGAGGTAGATCATCTTCAAGAGAGATCTCTT 714  
 241 ProGlyLeuLysGluProAlaAlaSerLeuHisSerGluSerProArgGlyLysSerSer 260  
 715 TCTGTCATCGACAGAGTCTCTGCATCTTTCATTTCAGAGAGACAGAGAGAGTAGT 774  
 261 LeuLeuValSerLeuArgThrHisMetSerGlySerIleAlaPheLysValGlySer 280  
 775 CTCATGTTTCTCTCAAGAACCAAGATGAATAGCAATACAAATTCCTTCCAAAATGGGTTC 834  
 281 PheCysArgSerGluSerProValLeuHisGlnArgGluHisValGluLeuLeuArgGly 300  
 835 TTCTCCCAATCAGATTCGTAGCTCTTCCAAAGGGAACATGTTGAACCTGCTTAGAGCC 894  
 301 ArgLysLeuAlaArgSerLeuAlaValLeuLeuSerAlaPheAlaIleCysTrpAlaPro 320  
 895 AGGAGATTAGCAAGTCACTGGCCATCTCTTAGGGGTTTTTGTCTGTTCTGGCTCCA 954  
 321 TyrCysLeuPheThrIleValLeuSerThrTyrArgGlyGluArgProLysSerIle 340  
 955 TATTCTCTGTTCACAAATTTGCTCTTTTCATTTTATTTCTCTCAGCAACAGGCTCTAAATCAGTT 1014  
 341 TrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerLeuIleLeuProPheLeuTyr 360  
 1015 TGGTATAGAAATTTGGCTTTCAGTGGTTCATTTCTTCTTGTCTCAATCTCTTTTGTAT 1074  
 361 ProLeuCysHisArgPheGlnLysAlaPheTrpLysIleLeuCysValThrLysGln 380  
 1075 CCATTGTGTCAAGGCGCTTTCAAAAGGCTTCTTGAATAATATTTGTATAAAAAGCAA 1134  
 381 ProAlaProSerGln---ThrGlnSerValSerSer 391

## Alignment Scores:

Pred. No.: 1.37e-119 Length: 1170  
 Score: 1403.50 Matches: 271  
 Percent Similarity: 79.34% Conservative: 40  
 Best Local Similarity: 69.13% Mismatches: 78  
 Query Match: 68.63% Indels: 3  
 DB: 9 Gaps: 2

US-10-626-126-9 (1-391) x AAD55126 (1-1170)

QY 1 MetSerGluSerAsnGlyThrAspValLeuProLeuThrAlaGlnValProLeuAlaPhe 20

Db 1 ATGCCGATACTAATAGCAACAATTTATCTAAGCACTCTGTGTTACTTTAGCAATT 60

DB 1135 CCTCTACCATCACACACAGTCGGTCAGTATCTTCT 1170  
 ||| ||||| ||| :|||: ||||| |||||

## RESULT 5

ID AAA46023 standard; cDNA; 1173 BP.  
 XX AC AAA46023;

DT 22-AUG-2000 (first entry)

XX DE Human G protein coupled receptor HRUP7 encoding cDNA SEQ ID NO:13.

XX KW Human; G protein coupled receptor; GPCR; transmembrane receptor;  
 KW identification; agonist; screening; therapeutic; pharmaceutical; mutant;  
 KW ss.

XX OS Homo sapiens.

XX PN WO200022131-A2.

XX PD 20-APR-2000.

XX PF 13-OCT-1999; 99WO-US024065.

XX PR 13-OCT-1998; 98US-00170496.

XX PR 12-NOV-1998; 98US-0108029P.

XX PR 20-NOV-1998; 98US-0109213P.

XX PR 27-NOV-1998; 98US-0110060P.

XX PR 16-FEB-1999; 99US-0120416P.

XX PR 26-FEB-1999; 99US-0121852P.

XX PR 12-MAR-1999; 99US-0123944P.

XX PR 12-MAR-1999; 99US-0123945P.

XX PR 12-MAR-1999; 99US-0123946P.

XX PR 12-MAR-1999; 99US-0123948P.

XX PR 12-MAR-1999; 99US-0123949P.

XX PR 12-MAR-1999; 99US-0123951P.

XX PR 28-MAY-1999; 99US-0136436P.

XX PR 28-MAY-1999; 99US-0136437P.

XX PR 28-MAY-1999; 99US-0136439P.

XX PR 28-MAY-1999; 99US-0137127P.

XX PR 28-MAY-1999; 99US-0137131P.

XX PR 28-MAY-1999; 99US-0137567P.

XX PR 29-JUN-1999; 99US-0141448P.

XX PR 27-AUG-1999; 99US-0151114P.

XX PR 29-SEP-1999; 99US-0154524P.

XX PR 29-SEP-1999; 99US-0156555P.

XX PR 29-SEP-1999; 99US-0156633P.

XX PR 29-SEP-1999; 99US-0156634P.

XX PR 29-SEP-1999; 99US-0156653P.

XX PR 01-OCT-1999; 99US-0157280P.

XX PR 01-OCT-1999; 99US-0157281P.

XX PR 01-OCT-1999; 99US-0157282P.

XX PR 01-OCT-1999; 99US-0157293P.

XX PR 01-OCT-1999; 99US-0157294P.

XX PR 12-OCT-1999; 99US-00416760.

XX PR 12-OCT-1999; 99US-00417044.

XX PA (AREN-) ARENA PHARM INC.

XX PI Behan DP, Lehmann-Bruinema K, Chalmers DT, Chen R, Dang HT;

XX PI Gore M, Liaw CW, Lin I, Lowitz K, White C;

XX DR WPI; 2000-317986/27.

XX DR F-PSDB; AAS02831.

XX PT Non-endogenous, human G protein-coupled receptors for screening receptor,

XX PT inverse or partial agonists useful as therapeutic agents.

XX XX Example 1; Page 88-89; 187pp; English.

XX XX The present invention describes transmembrane receptors, preferably human

XX CC G protein coupled receptors (GPCR), for which the endogenous ligand is

CC unknown (orphan GPCR receptors). More specifically the present invention  
 CC relates to non-endogenous, constitutively activated versions of a human  
 CC GPCR. These non-endogenous human GPCRs can be useful for the direct  
 CC identification of candidate compounds as receptors agonists, inverse  
 CC agonists or partial agonists for use as pharmaceutical agents. AAA46017  
 CC to AAA46126 and AAB02825 to AAB02859 represent sequences used in the  
 CC exemplification of the present invention

XX SQ Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.: 1.37e-119 Length: 1173  
 Score: 1403.50 Matches: 271  
 Percent Similarity: 79.34% Conservative: 40  
 Best Local Similarity: 69.13% Mismatches: 78  
 Query Match: 68.63% Indels: 3  
 DB: 3 Gaps: 2

US-10-626-126-9 (1-391) x AAA46023 (1-1173)

QY 1 MetSerGluSerAsnGlyThrAspValLeuProLeuThrAlaGlnValProLeuAlaPhe 20

DB 1 ATGCCAGATACATAATAGCACAAATCAATTTATCCTAAGCAGCTCGTGTACTTTAGCATTT 60

QY 21 LeuMetSerLeuLeuAlaPheAlaIleThrIleGlyAsnAlaValValIleLeuAlaPhe 40

DB 61 TTTATGCTCTAGTAGCTTTTGCTATATGCTAGGAAATGCTTTGGTCAATTTAGCTTTT 120

QY 41 ValAlaAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60

DB 121 GTGGTGGACAAAACCTTAGACATCGAAGTAGTATTATTTTCTTAACCTGGCCATCTCT 180

QY 61 AspPhePheValGlyValIleSerIleProLeuTyrIleProHisThrLeuPheAsnTrp 80

DB 181 GACTTCTTTGTGGGTGTGATCTCCATCTCTTTGTATCATCCCTCACACGCTGTTCGAATGG 240

QY 81 AsnProGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeuLeuCysThrAla 100

DB 241 GATTTTGGAAAGGAATCTGTGTATTTTGGTCACTACTGACTATCTGTATGTACAGCA 300

QY 101 SerValTyrSerIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120

DB 301 TCTGTATATAACATGTCTCATCAGCTATGATCATCAGTCTGCTCAAAATGCTGTG 360

QY 121 ArgTyrArgAlaGlnHisThrGlyIleLeuIleValAlaGlnMetValAlaValTrp 140

DB 361 TCTTATAGAACTCAACATACCTGGGTCTTGAAGATTGTACTCTGATGGTGGCCGTTTGG 420

QY 141 IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTrpIleAsnSer 160

DB 421 GTGCTGGCTTCTTAGTGAATGGGCCAATGATTTCTAGTTTCAGAGTCTTGGAGGATGNA 480

QY 161 ThrAsnThrGluGluCysGluProGlyPheValThrGluTrpTyrIleLeuAlaIleThr 180

DB 481 GGTAGT-----GAATGTGAACCTGGATTCTTTCGAATGGTACATCTCTGCCATCACA 534

QY 181 AlaPheLeuGluPheLeuLeuProValSerIleValValTyrPheSerValGlnIleTyr 200

DB 535 TCATTCTTGAATTCGTATCCAGTCTCTTAGTCGCTTATTTCAACATGAATATTTAT 594

QY 201 TrpSerLeuTrpIleAsnGlySerLeuSerArgCysProSerHisAlaGlyPheIleAla 220

DB 595 TGGAGCCTGTGGAGCGTGATCATCTCAGTAGTGGCAAGCCATCTCTGGACTGCTGCT 654

QY 221 ThrSerSerArgGlyThrGlyHisSerArgArgThrGlyLeuAlaCysArgThrSerLeu 240

DB 655 GTCTCTTCCAAACATCTGTGGACACTCATTCAGAGGTAGATATCTTCAAGGAGATCTCT 714

QY 241 ProGlyLeuLeuGluProAlaAlaSerLeuHisSerGluSerProArgGlyIleSerSer 260

DB 715 TCTGCATGCACAGAAGTCTCTGCATCTTTCATTCAGAGAGACAGAGGAGAGAGTAGT 774

QY 261 LeuLeuValSerLeuArgThrHisMetSerGlySerIleIleAlaPheIleValGlySer 280

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Db 775 TCATGTTTCTCAAGACCAAGATGAATACAAATGCTTCCAAAATGGTGCC 834
Qy 281 PheCysArgSerGluSerProValLeuHisGlnArgGluHisValGluLeuLeuArgGly 300
Db 835 TTCTCCAATCAGATTCGTAGCTCTTCACCAAGGGAACATGTTGAAGCTGTAGAGCC 894
Qy 301 ArgLysLeuAlaArgSerLeuAlaValLeuLeuSerAlaPheAlaIleCysTrpAlaPro 320
Db 895 AGGAGATTAGCCAAGTCACTGGCCATCTCTTAGGGGTTTTGCTGCTGGGCTCCA 954
Qy 321 TyrCysLeuPheThrIleValLeuSerThrTyrArgGlyGluArgProLysSerIle 340
Db 955 TATTCCTGTTCCAAATGCTCTTCATTTTATTCCTCAGCAACAGGCTCTAAATCAGTT 1014
Qy 341 TrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerLeuIleAsnProPheLeuTyr 360
Db 1015 TGGTATAGATTGCATTTGGCTTCAGTGGTTCATTCCTTTGTCATTCCTTTTGTAT 1074
Qy 361 ProLeuCysHisArgGlnPheGlnLysAlaPheTrpLysIleLeuCysValThrLysGln 380
Db 1075 CCATTGTGTCAAGCGCTTTCAAAGGCTTTCTTGAAAATATTTTGTATAAAAGCAA 1134
Qy 381 ProAlaProSerGln---ThrGlnSerValSerSer 391
Db 1135 CCTTACCATCAACACAGTCGGTCAGTATCTTCT 1170
RESULT 6
AAD01124
ID AAD01124 standard; cDNA; 1173 BP.
XX AAD01124;
XX
XX 02-NOV-2000 (first entry)
XX Human orphan G protein-coupled receptor hRUP7 cDNA.
XX
XX Human; orphan G protein-coupled receptor; GPCR; hRUP7; drug screening;
XX transmembrane receptor; signal cascade; ss.
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 1..1173
XX FT /*tag= a
XX FT /product= "hRUP7"
XX FT /note= "Human orphan G protein-coupled receptor"
XX
XX WO200031258-A2.
XX
XX 02-JUN-2000.
XX
XX 13-OCT-1999; 99WO-US023687.
XX
XX 20-NOV-1998; 98US-0109213P.
XX 16-FEB-1999; 98US-0120416P.
XX 26-FEB-1999; 99US-0121852P.
XX 12-MAR-1999; 99US-0123946P.
XX 12-MAR-1999; 99US-0123949P.
XX 28-MAY-1999; 99US-0136436P.
XX 28-MAY-1999; 99US-0136437P.
XX 28-MAY-1999; 99US-0136439P.
XX 28-MAY-1999; 99US-0136567P.
XX 28-MAY-1999; 99US-0137127P.
XX 28-MAY-1999; 99US-0137131P.
XX 29-JUN-1999; 99US-0141448P.
XX 29-SEP-1999; 99US-0156535P.
XX 29-SEP-1999; 99US-0156633P.
XX 29-SEP-1999; 99US-0156634P.
XX 29-SEP-1999; 99US-0156653P.
XX 01-OCT-1999; 99US-0157280P.
XX 01-OCT-1999; 99US-0157281P.
XX 01-OCT-1999; 99US-0157282P.
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PR 01-OCT-1999; 99US-0157293P.
PR 01-OCT-1999; 99US-0157294P.
PR 12-OCT-1999; 99US-00416760.
XX 12-OCT-1999; 99US-00417044.
PA (AREN-) ARENA PHARM INC.
XX
PI Chen R, Dang HT, Liaw CW, Lin I;
XX
DR WPI; 2000-400068/34.
DR P-PSDB; AAY11297.
XX
XX Novel human orphan G protein-coupled receptors and the encoding cDNAs for
XX use in the identification of G protein-coupled receptor agonists.
XX
XX Claim 25; Page 59; 102pp; English.
XX
XX The present sequence is a cDNA encoding hRUP7, an endogenous human orphan
XX G protein-coupled receptor (GPCR). The full length hRUP7 cDNA was cloned
XX by RT-PCR using human peripheral leucocyte cDNA as template. The orphan
XX GPCR of the invention, like all GPCRs has seven transmembrane alpha
XX helices with an extracellular N-terminus and an intracellular C-terminus.
XX However, no endogenous ligands has yet been identified for the proteins
XX of the invention. The orphan GPCRs may be used in the identification of
XX their endogenous ligands, and to screen potential GPCR agonists and
XX antagonists for use as pharmaceutical agents. The proteins may also be
XX used in the study of GPCR-mediated signalling cascades, and to elucidate
XX their precise role in normal and diseased human conditions. Nucleic acid
XX encoding human orphan GPCRs may be used for tissue localisation
XX expression analysis to provide information about their function in
XX healthy and pathological states
XX
XX Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;
XX
Alignment Scores:
Pred. No.: 1,37e-119 Length: 1173
Score: 1403.50 Matches: 271
Percent Similarity: 79.34% Conservative: 40
Best Local Similarity: 69.13% Mismatches: 78
Query Match: 68.63% Indels: 3
DB: 3 Gaps: 2
US-10-626-126-9 (1-391) x AAD01124 (1-1173)
Qy 1 MetSerGluSerAsnGlyThrAspValLeuProLeuThrAlaGlnValProLeuAlaPhe 20
Db 1 ATGCCAGATACATAAGCACAATCAATTTATCATTAGCACTCGTGTTACTTTAGCATTT 60
Qy 21 LeuMetSerLeuLeuAlaPheAlaIleThrIleGlyAsnAlaValIleLeuAlaPhe 40
Db 61 TTTATGTCTTAGTAGCTTTTGCTATAATGCTAGGAAATGCTTTGCTCATTTAGCTTTT 120
Qy 41 ValAlaAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60
Db 121 GTGGTGGACAAACCTTAGACATCGAAGTAGTATTATTTTCTTAACATGGCCATCTCT 180
Qy 61 AspPhePheValGlyValIleSerIleProLeuTyrIleProHisThrLeuPheAsnTrp 80
Db 181 GACTTCTTTTGGGTGTGATCTCCATTCTTTGTACATCCCTCACACGCTGTTCGATGG 240
Qy 81 AsnProGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeuLeuCysThrAla 100
Db 241 GATTTTGGAAAGGAAATCTGTGATTTTGGCTCAGTACTACTGACTATCTGTATGACGCA 300
Qy 101 SerValTyrSerIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120
Db 301 TCTGTATATAACATTGCTCTCATCAGCTATGATACCTGCTGACTCTCAATGCTGTG 360
Qy 121 ArgTyrArgAlaGlnHisThrGlyIleLeuLysIleValAlaGlnMetValAlaValTrp 140
Db 361 TCTTATAGAACTCAACATACCTGGGCTCTTGAGATTGTTACTCTGATGGTGGCGCTTGG 420
Qy 141 IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTrpLysAsnSer 160
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Db 421 GTGCTGGCCTTCTTAGTGAATGGCCCAATGATTCTAGTTTCAGAGTCTTGGAGGATCAA 480
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Qy 161 ThrAenThrGluGluCysGluProGlyPheValThrGluTrpTyrIleLeuAlaIleThr 180
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 481 GGTAGT-----GAATGTGAACCTGGATTTTTTTCGGAATGCTATCCTTGCCATCACA 534
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Qy 181 AlaPheLeuGluPheLeuLeuProValSerLeuValValTyrPheSerValGluIleTyr 200
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 535 TCATCTCTTGAATTCGATGCCAGTCACTTAGTCGCTTATTTCACATCAATATTATTTAT 594
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Qy 201 TrpSerLeuTrpLysArgGlySerLeuSerArgCysProSerHisAlaGlyPheIleAla 220
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 595 TGGAGCCTGTGAAGCGTGATCATCTCAGTAGGTGCCAAAGCCATCCTGGAGTCACTGCT 654
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Qy 221 ThrSerSerArgGlyThrGlyHisSerArgArgThrGlyLeuAlaCysArgThrSerLeu 240
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 655 GTCTCTTCCAAACATCTGTGGACACTCATTCAGAGGTAGACTATCTTCAAGGAGATCTCTT 714
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Qy 241 ProGlyLeuLysGluProAlaAlaSerLeuHisSerGluSerProArgGlyLysSerSer 260
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 715 TCTGATCGACAGAAGTTCCTGCTATCTTCTTTCAGAGACACAGAGGAGAAAGATAGT 774
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Qy 261 LeuLeuValSerLeuArgThrHisMetSerGlySerIleIleAlaPheLysValGlySer 280
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 775 CTCATGTTTCTCACAAGCAACCAAGATGAATAGCAATACATATGCTTCCAAATGGTTCC 834
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Qy 281 PheCysArgSerGluSerProValLeuHisGlnArgGluHisValGluLeuLeuArgGly 300
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Db 835 TTCTCCCAATCAGATTCTGTAGCTCTTCCACCAAGGGAACATGTTGMACTGCTTAGAGCC 894
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Qy 301 ArgLysLeuAlaArgSerLeuAlaValLeuLeuSerAlaPheAlaIleCysTrpAlaPro 320
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 895 AGGAGATTAGCCAGTCACTGCGCAATCTCTTAGGGGTTTGTGTTGCTGGGCTCCA 954
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Qy 321 TyrCysLeuPheThrIleValLeuSerThrTyrArgArgGlyGluArgProLysSerIle 340
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 955 TATTCTCTGTTCCAAATGTCTTTCATTTATTTCTCAGCAACAGGTCCTTAATCAGTT 1014
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Qy 341 TrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerLeuIleAsnProPheLeuTyr 360
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 1015 TGGTATAGAAATGCAATTTGGCTTCAGTGGTTCAATCTCTTGTCAATCTCTTTTGTAT 1074
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Qy 361 ProLeuCysHisArgArgPheGlnLysAlaPheTrpLysIleLeuCysValThrLysGln 380
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 1075 CCATGTGTCAACGCGTTTCCAAAGGCTTCTTGAATAATATTTTGTATAAAAGCAA 1134
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::

Qy 381 ProAlaProSerGln---ThrGlnSerValSerSer 391
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 1135 CCTCTACCATCAACACAGTCGGTCAGTATCTTCT 1170
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::

RESULT 7
ID AAF83203 standard; cDNA; 1173 BP.
AC AAF83203;
XX
XX
XX 09-JUL-2001 (first entry)
XX
XX Human GPCR-like polypeptide, PFI-013 encoding cDNA.
XX
XX G-protein coupled receptor; GPCR; PFI-013; antiallergic; antiaesthetic;
KW antiinflammatory; vasotropic; antidiabetic; anorectic; cytostatic; human;
KW osteopathic; neuroprotective; nootropic; dermatological; gynecological;
KW signal transduction; ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 1..1173
XX FT /*tag= a
XX FT /product= "PFI-013"
XX

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PN EP1096009-A1.
XX
PD 02-MAY-2001.
XX
PF 24-OCT-2000; 2000EP-00309364.
XX
PR 29-OCT-1999; 99GB-00025641.
XX
PR 20-APR-2000; 2000GB-00009973.
XX
XX (PFI-013) PFIZER LTD.
XX (PFI-013) PFIZER INC.
XX
XX Peter B, O'reilly MA;
XX
XX WPI; 2001-309854/33.
XX P-PSDB; AAB62445.
XX
XX New G-protein coupled receptor-like polypeptide, polynucleotide for
XX screening drug candidates for treating diseases associated with signal
XX transduction e.g. allergic, inflammatory, pulmonary, neoplastic diseases.
XX
XX Claim 1; Page 43; 66pp; English.
XX
XX This cDNA of NCIMB 41073 encodes a human G-protein coupled receptor
XX (GPCR)-like polypeptide, designated PFI-013. The PFI-013 protein can be
XX expressed by standard recombinant methodology. Antibodies and modulators
XX of PFI-013 are useful in the manufacture of a medicament for treating
XX allergic disorder, including extrinsic asthma, immunological disorders,
XX such as intrinsic asthma, vasculitic granulomatous disease, interstitial
XX and other pulmonary disease, including chronic obstructive pulmonary
XX disease (COPD), infectious, inflammatory disease, such as inflammatory
XX bowel disease and neoplastic and myeloproliferative diseases. They are
XX also useful for treating obesity, diabetes, metabolic, neurological
XX diseases, psychotherapeutics, urogenital disease, reproduction and sexual
XX medicine, inflammation, cancer, tissue repair, dermatology, photoaging,
XX skin pigmentation, osteoporosis, cardiovascular, gastrointestinal
XX diseases, allergy and respiratory disease, sensory organ disorders, sleep
XX disorders and hair loss. The PFI-013 protein and nucleic acid are useful
XX in the diagnosis and treatment of the above conditions and also for
XX screening drug candidates for the treatment of diseases associated with
XX signal transduction. The antibodies are also useful for enrichment of
XX eosinophils from mammalian, especially human blood and for detecting the
XX protein in biological samples
XX
XX SQ Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.37e-119 Length: 1173
Score: 1403.50 Matches: 271
Percent Similarity: 79.34% Conservative: 40
Best Local Similarity: 69.13% Mismatches: 78
Query Match: 68.63% Indels: 3
DB: 4 Gaps: 2

US-10-626-126-9 (1-391) x AAF83203 (1-1173)
Qy 1 MetSerGluSerAsnGlyThrAspValLeuProLeuThrAlaGlnValProLeuAlaPhe 20
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Qy 21 LeuMetSerLeuLeuAlaPheAlaIleThrIleGlyAsnAlaValValIleLeuAlaPhe 40
Db 61 TTTATGCTTAGTAGCTTTTGTATATATGCTAGGAATGCTTTGGTCACTTTTACCTTT 120
Qy 41 ValAlaAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60
Db 121 GTGGTGGACAAAACCTTAGACATCGAAGTAGTATTTTCTTAACTTGGCCATCTCT 180
Qy 61 AspPhePheValGlyValIleSerIleProLeuTyrIleProHisThrLeuPheAsnTrp 80
Db 181 GACTTCTTTGGGGTGTGATCTCCATCTCTTTGTACATCCCTCACACCTGTTCGAATGG 240
Qy 81 AsnProGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeuLeuCysThrAla 100

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Db 241 GATTTTGGAAAGAAATCTGTGATTTTGGCTCACTACTGATCTGTATGTATACAGA 300
Qy 101 SerValTyrSerIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120
Db 301 TCTGTATATAACATGTTCTCTCATCAGCTATGATCGATCTGCTCAGTCTCAATGCTGTG 360
Qy 121 ArgTyrArgAlaGlnHisThrGlyIleLeuLeuIleValAlaGlnMetValAlaValTyr 140
Db 361 TCTTATAGAACTCAACATACCTGGGTCTTGAAGATTGTTACTCTGATGCTGGCCGCTTGG 420
Qy 141 IleLeuAlaPheIleuValAnglyProMetIleLeuAlaSerAspSerTrpIysAsnSer 160
Db 421 GTGCTGGCCCTTCTTAGTGAATGGCAATGATTTCTAGTTTTCAGAGTCTTGGAGGATGAA 480
Qy 161 ThrAsnThrGluGluCysGluProGlyPheValThrGluTrpTyrIleLeuAlaIleThr 180
Db 481 GGTAGT-----GAATGTGACCTGGATTTTTCGGAATGGTACATCTTCCCATCACA 534
Qy 181 AlaPheLeuGluPheLeuLeuProValSerLeuValValTyrPheSerValGlnIleTyr 200
Db 535 TCATTTCTTGAATTCGTGATCCAGTCACTCTAGTCGCTTATTTCAACATGAATATTAT 594
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Db 595 TGGAGCCTGTGAAGCGTGCATCATCTCAGTAGTGCCAAAGCCATCTCTGAGCTGCTGT 654
Qy 221 ThrSerSerArgGlyThrGlyHisSerArgArgThrGlyLeuAlaCysArgThrSerLeu 240
Db 655 GTCTCTTCCACACTGTGTGACACTCATTCAGAGGTAGACTATCTTCAAGGAGATCTCT 714
Qy 241 ProGlyLeuLeuGluProAlaLeuAlaSerLeuHisSerGluSerProArgGlyIysSer 260
Db 715 TCTGCATCAGACAGAAGTCTCTGCATCTTTCATTTCAGAGAGACAGAGGAGAAAGTAGT 774
Qy 261 LeuLeuValSerLeuArgThrHisMetSerGlySerIleIleAlaPheIysValGlySer 280
Db 775 CTCATGTTTCTCAAGAACCAAGATGATGATAGCAATACAAATTCCTCCAAATGGGTTC 834
Qy 281 PheCysArgSerGluSerProValLeuHisGlnArgGluHisValGluLeuLeuArgGly 300
Db 835 TTCCTCCATCAGATTTCTGTAGCTCTTCCAAAGGAGACATGTTGAGCTGCTTAGAGCC 894
Qy 301 ArgLysLeuAlaArgSerLeuAlaValLeuLeuSerAlaPheAlaIleCysTrpAlaPro 320
Db 895 AGGAGATTAGCAAGTCACTGGCCATCTCTTAGGGGTTTTTCTGTTGCTGGCTCCA 954
Qy 321 TyrCysLeuPheThrIleValLeuSerThrTyrArgArgGlyGluArgProIysSerIle 340
Db 955 TATTCTCTGTTCACAAATGTCCTTTCATTTATTCCTCAGCAACAGGTCCTAAATCAGTT 1014
Qy 341 TrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerLeuIleAsnProPheLeuTyr 360
Db 1015 TGTATAGAAATTCATTTGGCTTCAGTGGTTCATTCCTTTGTCATCTCTTTTGTAT 1074
Qy 361 ProLeuCysHisArgArgPheGlnLysAlaPheTrpIysIleLeuCysValThrLysGln 380
Db 1075 CCATTGTGTCAAGCGCTTCAAAAGGCTTTCTGAAATATTTTGTATATAAAAGCAA 1134
Qy 381 ProAlaProSerGln---ThrGlnSerValSerSer 391
Db 1135 CCTCTACCATCACACACAGCTCGGTAGTATCTTCT 1170
RESULT 8
AAH24007
ID AAH24007 standard; cDNA; 1173 BP.
AC AAH24007;
XX
DT 10-AUG-2001 (first entry)
XX
DE Human G protein-coupled receptor AXOR35 cDNA.
XX
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KW AXOR35; human; G protein-coupled receptor; 7TM receptor;
KW histamine H3 receptor homologue; infection; viral; bacterial; fungal;
KW protozoan; HIV-1; HIV-2; pain; cancer; diabetes; obesity; anorexia;
KW bulimia; osteoporosis; asthma; allergy; urinary retention;
KW acute heart failure; hypotension; hypertension; angina pectoris;
KW myocardial infarction; stroke; ulcer; migraine; vomiting;
KW psychotic disorder; neurological disorder; anxiety; schizophrenia;
KW manic depression; bipolar disorder; depression; delirium; dementia;
KW severe mental retardation; dyskinesia; Parkinson's disease;
KW Huntington's disease; Gilles de la Tourette's syndrome; lymphocyte;
KW macrophage; eosinophil; neutrophil; function modulation;
KW autoimmune disorder; pulmonary disorder; gene therapy; vaccine;
KW drug screening; signal transduction; transgenic animal; drug discovery;
KW ss.
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 1..1173
XX /tag= a
XX /product= "Human AXOR35"
XX /note= "G protein-coupled receptor"
XX
XX WO200133221-A1.
XX
XX 10-MAY-2001.
XX
XX 26-OCT-2000; 2000WO-US029461.
XX
XX 02-NOV-1999; 99US-00431898.
XX 03-FEB-2000; 2000US-00497790.
XX
XX (SMIK ) SMITHKLINE BEECHAM CORP.
XX (SMIK ) SMITHKLINE BEECHAM PLC.
XX
XX Aubart KM, Bergsma DJ, Fitzgerald LR, Graybill TL, Li X;
XX Michalovich D, Morrow DW, Zhu Y;
XX WPI; 2001-316464/33.
XX P-PSDB; AAB73622.
XX
XX Novel G-protein coupled receptor polypeptide and polynucleotide for
XX treating cancer, autoimmune, pulmonary, cardiovascular and neurological
XX disorders and for identifying modulators useful for treating asthma.
XX
XX Claim 2; Page 49-50; 54pp; English.
XX
XX The invention relates to the human G protein-coupled receptor AXOR35
XX (AAB73621), to cDNA encoding AXOR35 (AAH24006), and to AXOR35 fragments
XX and variants. Like all G protein-coupled receptors, AXOR35 has 7 putative
XX transmembrane domains and is involved in signal transduction. AXOR35 has
XX homology and structural similarity with G protein-coupled receptors such
XX as the human histamine H3 receptor. The invention also relates to
XX expression vectors and host cells comprising AXOR35 DNA, to recombinant
XX expression of AXOR35, and to an AXOR35-specific antibody. AXOR35 proteins
XX and nucleotides may be used to treat a wide variety of disorders
XX including bacterial, fungal, protozoal and viral infections, particularly
XX HIV-1 or HIV-2 infections; pain; cancers; benign prostatic hypertrophy;
XX diabetes; obesity; anorexia; bulimia; osteoporosis; asthma; allergies;
XX urinary retention; acute heart failure; hypotension; hypertension; angina
XX pectoris; myocardial infarction; stroke; ulcers; migraine; vomiting;
XX psychotic and neurological disorders such as anxiety, schizophrenia,
XX manic depression, depression, delirium, dementia, and severe mental
XX retardation, and dyskinesias, such as Parkinson's disease, Huntington's
XX disease or Gilles de la Tourette's syndrome. AXOR35 proteins and
XX nucleotides are useful as vaccines, and AXOR35 proteins, nucleotides and
XX antibodies may be used in screening compounds for their ability to
XX modulate AXOR35 activity or expression. Such AXOR35 modulators are
XX particularly useful for treating asthma, and inhibiting or promoting the
XX function of lymphocytes, macrophages, eosinophils or neutrophils in
XX asthmatic lung. AXOR35 proteins, nucleotides and antibodies are also
XX useful for diagnosing or determining susceptibility of an individual to a
XX disease via the detection of abnormal levels of protein or mRNA, or via
```



CC the detection of mutations in the corresponding gene. AXOR35 proteins are  
 CC also useful for inducing an immunological response in a mammal against  
 CC the above diseases, and for antibody production. AXOR35 nucleotides are  
 CC also useful as diagnostic reagents, in chromosome localisation and tissue  
 CC expression studies, and for producing transgenic animals useful in drug  
 CC discovery. AXOR35-specific antibodies are useful for purifying the AXOR35  
 CC protein or fragments thereof, and are also useful for treating conditions  
 CC associated with the expression of the AXOR35 protein. The present  
 CC sequence represents cDNA encoding human AXOR35

XX  
 SQ Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;

#### Alignment Scores:

Pred. No.: 1,37e-119 Length: 1173  
 Scores: 1403.50 Matches: 271  
 Percent Similarity: 79.34% Conservative: 40  
 Best Local Similarity: 69.13% Mismatches: 78  
 Query Match: 68.63% Indels: 3  
 DB: 5 Gaps: 2

US-10-626-126-9 (1-391) x AAU24007 (1-1173)

Qy 1 MetSerGluSerAsnGlyThrAspValLeuProLeuThrAlaGlnValProLeuAlaPhe 20  
 Db 1 ATGCCAGATACATAATAGCACAAATCAATTTATCACTAAGCACTCGGTACTTTAGCAATTT 60  
 Qy 21 LeuMetSerLeuAlaPheAlaPheAlaPheAlaPheAlaPheAlaPheAlaPheAlaPhe 40  
 Db 61 TTTATGTCCTTAGTAGCTTTTGTCTATAATGCTAGAGAAATGCTTTGCTATTAGCTTTT 120  
 Qy 41 ValAlaAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaPheSer 60  
 Db 121 GTGGTGGCAAAACCTTAGACATCGAAGTAGTATTTTCTTAACCTGGCCATCTCT 180  
 Qy 61 AspPhePheValGlyValIleSerIleProLeuTyrIleProHisThrLeuPheAsnTrp 80  
 Db 181 GACTTCTTTGTGGGTGTGATCTCCATTCCTTTGTATCATCTCCCTCACAGCTGTCGAATGG 240  
 Qy 81 AsnProGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrIleLeuCysThrAla 100  
 Db 241 GATTTTGGAAAGGAATCTGTATTTTGGCTCCTACTACTGACTATCTGTATGTACACGA 300  
 Qy 101 SerValTyrSerIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120  
 Db 301 TCTGTATATAATCTCTCATCAGCATGATCATACCTGCTAGCTCAAACTGCTGTG 360  
 Qy 121 ArgTyrArgAlaGlnHisThrGlyIleLeuIleValAlaGlnMetValAlaValTrp 140  
 Db 361 TCTTATAGAACTCAACATACCTGGGTCTTGAAGATTGTACTCTGATGGTGGCCGTTTG 420  
 Qy 141 IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTrpIleAsnSer 160  
 Db 421 GTGCTGGCCCTCTTAGTGAATGGGCAATGATCTAGTTTTCAGATCTTGGGAAGATGAA 480  
 Qy 161 ThrAsnThrGluGluCysGluProGlyPheValThrGluTyrTyrIleLeuAlaIleThr 180  
 Db 481 GGATG-----GAATGGAACCTGGATTTTTCGGAATGGTATATCTCTCCATCACA 534  
 Qy 181 AlaPheLeuGluPheLeuProValSerLeuValValTyrPheSerValGlnIleTyr 200  
 Db 535 TCATCTTTGGAATTCGTGATCCAGTCATCTTAGTCGCTTATTTCAACATGAATATTTAT 594  
 Qy 201 TrpSerLeuTyrPheArgGlySerLeuSerArgCysProSerHisAlaGlyPheIleAla 220  
 Db 595 TGGAGCCCTGTGAAGCGGATCATCTCAGTAGGTGCCAAAGCCCTCTGAGCTGACTGCT 654  
 Qy 221 ThrSerSerArgGlyThrGlyHisSerArgArgThrGlyLeuAlaCysArgThrSerLeu 240  
 Db 655 GTCTCTTCCAACATCTGTGGACACTCATTCAGAGGTAGATATCTTCAAGGAGATCTCT 714  
 Qy 241 ProGlyLeuLysGluProAlaAlaSerLeuHisSerGluSerProArgGlyIleSerSer 260  
 Db 715 TCTGCATCGACAGAGTTCTCTGCATCTCTTCTTCTTCTCAGAGAGACAGAGAGAGAGTAGT 774

Qy 261 LeuLeuValSerLeuArgThrHisMetSerGlySerIleIleAlaPheIleValGlySer 280  
 Db 775 CTCATGTTTTCTCAAGAACCAAGATGAATAGCAATACAAATGCTTCCAAATGGGTTC 834  
 Qy 281 PheCysArgSerGluSerProValLeuHisGlnArgGluHisValGluLeuLeuArgGly 300  
 Db 835 TTTCTCCCAATCAGATTCCTAGCTCTTCAACCAAGGGAACATGTTGAATCTGCTTAGACC 894  
 Qy 301 ArgIleLeuAlaArgSerLeuAlaValLeuLeuSerAlaPheAlaIleCysTrpAlaPro 320  
 Db 895 AGGAGATTAGCAAGTCACTGCCCATCTCTTAGGGGTTTTTGTCTGTCTTGTGGGCTCCA 954  
 Qy 321 TyrCysLeuPheThrIleValLeuSerThrTyrArgArgGlyGluArgProIleSerIle 340  
 Db 955 TATTCTCTGTGTACAAATGTCCTTTTCATTTATTCCTCAGCAACAGGTCCTTAAATCAGTT 1014  
 Qy 341 TrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerLeuIleAsnProPheLeuTyr 360  
 Db 1015 TGGTATAGAAATGCAATTTTGGCTTCAGTGGTTCATTCCTTGTCAATCTCTTTGTAT 1074  
 Qy 361 ProLeuCysHisArgArgPheGlnIleValPheTrpIleLeuCysValThrIleGln 380  
 Db 1075 CCATTGTGTCAACAGCGCTTCAAAAGGCTTCTTGAATAATATTTGTATATAAAAGCAA 1134  
 Qy 381 ProAlaProSerGln---ThrGlnSerValSerSer 391  
 Db 1135 CCTTACCATCACACACAGTCGGTCACTATCTTCT 1170

RESULT 9  
 ABZ80663  
 ID ABZ80663 standard; cDNA; 1173 BP.  
 XX  
 AC ABZ80663;  
 XX  
 DT 13-JUN-2003 (first entry)  
 XX  
 DE Human histamine receptor coding sequence.  
 XX  
 KW human; histamine receptor; gene; ds; chromosome 18; anti-inflammatory;  
 KW anti-migraine; anti-allergic; dermatological; cerebroprotective; stroke;  
 KW anti-migraine; cardant; anti-rheumatic; anti-arthritis; antipsoriatic;  
 KW neuroprotective; inflammation; asthma; allergy; atopic dermatitis;  
 KW myocardial infarction; migraine; chronic obstructive pulmonary disease;  
 KW rheumatoid arthritis; multiple sclerosis; inflammatory bowel disease;  
 KW psoriasis; receptor.  
 OS Homo sapiens.  
 PH Key Location/Qualifiers  
 FT CDS 1..1173  
 FT /\*tag= a  
 FT /product= "Histamine receptor"  
 XX  
 PN US6204017-B1.  
 XX  
 PD 20-MAR-2001.  
 XX  
 PF 07-OCT-1999; 99US-00414010.  
 XX  
 PR 07-OCT-1999; 99US-00414010.  
 XX  
 PA (SCHE ) SCHERING CORP.  
 XX  
 PI Behan JX, Hedrick JA, Laz TM, Monema PJ, Morse KL, Umland SP;  
 PI Wang S;  
 XX  
 DR WPI: 2002-442063/47.  
 XX  
 DR P-PSDB; AB098629.  
 XX  
 PT New nucleic acid encoding antigenic part of human histamine receptor,  
 PT useful for preparing antibodies, e.g. for treating-histamine related  
 PT disorders.



XX Example 1; Col 27-28; 19pp; English.

XX This sequence represents the open reading frame for a human histamine  
 CC receptor (HR) designated SP9144. The sequence was isolated by searching  
 CC databases with the sequence of known G-coupled protein receptor (GPCR).  
 CC The gene is used for recombinant production of HR and for preparing  
 CC antibodies (Ab). These Ab are used to purify HR by immunofluorescence  
 CC chromatography, in immunosay of histamine receptor, to identify cDNA  
 CC clones that express the receptor, as antagonist to block binding of  
 CC histamine (for treating any histamine-associated disorder) and to  
 CC generate anti-idiotypic antibodies. Agonists and antagonists of the HR  
 CC protein can be used in the treatment of e.g. inflammation, asthma,  
 CC allergy, atopic dermatitis, stroke, myocardial infarction, migraine,  
 CC chronic obstructive pulmonary disease, rheumatoid arthritis, multiple  
 CC sclerosis, inflammatory bowel disease and psoriasis

XX Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;

#### Alignment Scores:

Pred. No.: 1.37e-119 Length: 1173  
 Score: 1403.50 Matches: 271  
 Percent Similarity: 79.34% Conservative: 40  
 Best Local Similarity: 69.13% Mismatches: 78  
 Query Match: 68.63% Indels: 3  
 DB: 6 Gaps: 2

US-10-626-126-9 (1-391) x ABZ80663 (1-1173)

QY 1 MetSerGluSerAsnGlyThrAspValLeuProLeuThrAlaGlnValProLeuAlaPhe 20  
 DB 1 ATGCCAGATTAACCTAGACATCAATTTATCTAAGCACTCTGTTACTTTAGCATTT 60  
 QY 21 LeuMetSerLeuAlaPheAlaIleThrIleGlyAsnAlaValValIleLeuAlaPhe 40  
 DB 61 TTTATGCTCTAGTACTTTTCTATATGCTAGGAATGCTTTGCTCAATTTAGCTTTT 120  
 QY 41 ValAlaAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60  
 DB 121 GTGGTGGCAAAACCTTAGACATCGAAGTAGTATTTTCTTAACCTGGCATCTCT 180  
 QY 61 AspPheValGlyValIleSerIleProLeuTyrIleProHisThrIlePheAsnTyr 80  
 DB 181 GACTCTTTTGGTGGTGTATCTCCATTTCTGTATCCCTCACAGCTGTTTCGAATGG 240  
 QY 81 AsnProGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeuLeuCysThrAla 100  
 DB 241 GAATTTGGAAAGGAATCTGTATTTTGGCTCACTACTGACTATCTGTATGTAGCAGA 300  
 QY 101 SerValTyrSerIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120  
 DB 301 TCTGTATATAACATTGCTCTCATCAGTATGATCGATACCTGTCAAGTCTCAAAATGCTGTG 360  
 QY 121 ArgTyrArgAlaGlnHisThrGlyIleLeuLeuValIleValAlaGlnMetValAlaValTrp 140  
 DB 361 TCTTATAGAACTCAACATATCGGGTCTTTGAAGATTGTTACTCTGATGGCGCGTTGG 420  
 QY 141 IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTrpLysAsnSer 160  
 DB 421 GTGCTGGCTCTTCTAGTGAATGGCCAAATGATTTCTAGTTTCAGAGTCTTGAAGGATGAA 480  
 QY 161 ThrAsnThrGluGluCysGluProGlyPheValThrGluTrpTyrIleLeuAlaIleThr 180  
 DB 481 GGTAGT-----GAATGTGAACCTGGATTTTTCGGAATGGTATCTCTTGCATCACA 534  
 QY 181 AlaPheLeuGluPheLeuLeuProValSerLeuValValTyrPheSerValGlnIleTyr 200  
 DB 535 TCATTCTGGAAATTCGATGCCAGTCACTCTAGTCGCTTTATTTCAACATGAAATATTAT 594  
 QY 201 TrpSerLeuTrpLysArgGlySerLeuSerArgCysProSerHisAlaGlyPheIleAla 220  
 DB 595 TGGAGCTGTGGAGGCGTGATCATCTCAGTAGGTGGCAAGCCATCTCTGACTGACTGCT 654

QY 221 ThrSerSerArgGlyThrGlyHisSerArgArgThrGlyLeuAlaCysArgThrSerLeu 240  
 DB 655 GTCTCTTCCAAACATCTGTGGACACTCATTCACAGGTAGATGATTCACAGGAGATCTCTT 714  
 QY 241 ProGlyLeuLysGluProAlaIleSerLeuHisSerGluSerProArgGlyLysSerSer 260  
 DB 715 TCTGTCATCGACAGAGTCTCTGATCCTTTCATTTCAGAGACAGAGAGAGAGAGTAGT 774  
 QY 261 LeuLeuValSerLeuArgThrHisMetSerGlySerIleIleAlaPheLysValGlySer 280  
 DB 775 CTCATGTTTCTCTCAAGAACCAAGATGAATAGCAATACAAATGCTTCCAAAATGGGTTC 834  
 QY 281 PheCysArgSerGluSerProValLeuHisGlnArgGluHisValGluLeuLeuArgGly 300  
 DB 835 TTCTCCCAATCAGATTCTGTAGCTCTTCACCAAGGGAAACATGTTCAACTGCTTAGAGCC 894  
 QY 301 ArgLysLeuAlaArgSerLeuAlaValLeuLeuSerAlaPheAlaIleCysTrpAlaPro 320  
 DB 895 AGAGATTAGCCCAAGTCACTGCTCTTAGGGGTTTTCGCTGTTGCTGGGTCCA 954  
 QY 321 TyrCysLeuPheThrIleValLeuSerThrTyrArgArgGlyGluArgProLysSerIle 340  
 DB 955 TATTCCTCTCTTCAAAATGCTCTTTCATTATTTCTCAGCAACAGGTCTCTAAATCAGTT 1014  
 QY 341 TrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerLeuIleAsnProPheLeuTyr 360  
 DB 1015 TGGTATAGAAATGCAATTTTGGCTTCAAGTGGTTCATTTCTGCTCAATCTCTTTGTAT 1074  
 QY 361 ProLeuCysHisArgArgPheGlnLysAlaPheTrpLysIleLeuCysValThrLysGln 380  
 DB 1075 CCATTGTGTCAACAGCGCTTTCNAAGGCTTCTTGAAAATATTTTGTATAAAAAGCAA 1134  
 QY 381 ProAlaProSerGln---ThrGlnSerValSerSer 391  
 DB 1135 CCTTACCATTACACACACAGTCGGTCAGTATCTCT 1170  
 RESULT 10  
 ABQ78739  
 ID ABQ78739 standard; DNA; 1173 BP.  
 XX AC ABQ78739;  
 XX DT 05-DEC-2002 (first entry)  
 XX DE Nucleotide sequence of human histamine receptor.  
 XX KW Human; histamine receptor; receptor; inflammation; asthma; allergy;  
 KW atopic dermatitis; stroke; myocardial infection; migraine;  
 KW chronic obstructive pulmonary disease; COPD; rheumatoid arthritis;  
 KW multiple sclerosis; inflammatory bowel disease; psoriasis;  
 KW intracellular second messenger pathway; cellular growth rate;  
 KW hormone secretion; gene; ss.  
 XX OS Homo sapiens.  
 XX FH Key Location/Qualifiers  
 FT CDS 1..1173  
 FT FT /tag= a  
 FT FT /product= "histamine receptor"  
 XX US2002098539-A1.  
 XX PD 25-JUL-2002.  
 XX PF 19-MAR-2001; 2001US-00812216.  
 XX PR 07-OCT-1999; 99US-00414010.  
 XX (BEHA/) BEHAN J X.  
 XX (HEDR/) HEDRICK J A.  
 XX (LAZT/) LAZ T M.  
 XX (MONS/) MONSMA P J.  
 XX (MORS/) MORSE K L.



```

XX
PI Lovenberg T, Liu C;
XX WPI; 2002-114339/15.
DR P-PSDB; AAM50564.
XX
XX New mammalian histamine H4 receptor proteins and polynucleotides encoding
PT the proteins, useful in gene therapy for treating diseases where it is
PT beneficial to elevate mammalian histamine H4 receptor activity.
XX
XX Claim 4; Fig 1; 92pp; English.
XX
XX The present sequence is that of cDNA clone pH4R encoding a human
CC histamine receptor of the H4 subtype. The cDNA was isolated from a bone
CC marrow cDNA library. The invention provides mammalian (human, mouse, rat
CC and guinea pig) histamine H4 receptor nucleic acid molecules (see
CC AAI70980-83) and polypeptides (see AAM50564-67). The nucleic acids have
CC been expressed in recombinant host cells that produce active recombinant
CC protein. The pharmacology of known histamine ligands is demonstrated.
CC Mammalian histamine H4 receptor may be used in gene therapy for the
CC treatment of diseases where it is beneficial to elevate mammalian
CC histamine H4 receptor activity. Recombinant protein is useful for
CC identifying modulators of the human histamine H4 receptor. Such
CC modulators may be useful for diagnosing, treating or preventing asthma,
CC allergy, inflammation, cardiovascular and cerebrovascular disorders, non-
CC insulin dependent diabetes mellitus, hyperglycemia, constipation,
CC arrhythmia, disorders of the neuroendocrine system, stress and spasticity
XX
SQ Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.37e-119 Length: 1173
Score: 1403.50 Matches: 271
Percent Similarity: 79.34% Conservative: 40
Best Local Similarity: 69.13% Mismatches: 78
Query Match: 68.63% Indels: 3
DB: 6 Gaps: 2

US-10-626-126-9 (1-391) x AAI70980 (1-1173)

QY 1 MetSerGluSerAsnGlyThrAspValLeuProLeuThrAlaGlnValProLeuAlaPhe 20
DB 1 ATGCCAGTACTAATAGCAACAATCAATTTATCACTAAGCACTCGTGTACTTTAGCATTT 60
QY 21 LeuMetSerLeuLeuAlaPheAlaIleThrIleGlyAsnAlaValValIleLeuAlaPhe 40
DB 61 TTTATGCTCTTAGTAGCTTTTGCTATAATGCTAGGAAATGCTTTGCTCATTTAGCTTTT 120
QY 41 ValAlaAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60
DB 121 GTGGTGGACAAACCTTAGACATCGAAGTAGTATTATTTTCTTAACCTGGCCATCTCT 180
QY 61 AspPhePheValGlyValIleSerIleProLeuTyrIleProHisThrLeuPheAsnTrp 80
DB 181 GACTCTTTTGGGTGTGATCTCCATCTCTTGATATCCCTCACAGCTGTTGCAATGG 240
QY 81 AsnProGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeuLeuCysThrAla 100
DB 241 GATTTTGGAAAGGAATCTGTGATTTTGGCTCACTACTACTGACTATCTGTATGTACAGCA 300
QY 101 SerValTyrSerIleValleuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120
DB 301 TCTGTATATAACATGCTCCATCATCAGCTATGATCGATACCTGTCAGTCTCAAAATGCTGTG 360
QY 121 ArgTyrArgAlaGlnHisThrGlyIleLeuValIleValAlaGlnMetValAlaValTrp 140
DB 361 TCTTATAGAACTCAACATACCTGGGCTTGAAGATTGTACTCTGATGGTGGCGGTTGG 420
QY 141 IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTrpIlyAsnSer 160
DB 421 GTCTGGCCCTCTTAGTGAATGGCCCAATGATTTCTAGTTTCAGATCTTGGAGGATGAA 480
QY 161 ThrAsnThrGluGluCysGluProGlyPheValThrGluTrpTyrIleLeuAlaIleThr 180

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Db 481 GGTAGT-----GAATGTGAACCTGGATTTTTCGGAATGGTACATCTCTTGCATCACA 534
QY 181 AlaPheLeuGluPheLeuProValSerLeuValValTyrPheSerValGlnIleTyr 200
Db 535 TCATTTCTTGGAAATCTGTGATCCAGTCATCTTAGTCGCTTATTTCAACATGAATATTTAT 594
QY 201 TrpSerLeuTrpIlyAsnGlySerLeuSerArgCysProSerHisAlaGlyPheIleAla 220
Db 595 TGGAGCCTGTGGAAGCGTGATCATCTCAGTAGGTGCAAGCCATCTCTGGACTGACTGCT 654
QY 221 ThrSerSerArgGlyThrGlyHisSerArgArgThrGlyLeuAlaCysArgThrSerLeu 240
Db 655 GTCTCTTCAACATCTGTGGACACTCATTTCAAGAGGTAGACTATCTTCAAGGAGATCTCTT 714
QY 241 ProGlyLeuLysGluProAlaIleSerLeuHisSerGluSerProArgGlyLysSerSer 260
Db 715 TCTGCATCACAGAGAGTTCTCTGCATCTTCAATTCAGAGACAGAGAGAGAGTAGT 774
QY 261 LeuLeuValSerLeuArgThrHisMetSerGlySerIleIleAlaPheLysValGlySer 280
Db 775 CTCATGTTTCTCAAGAACCAAGATGAATAGCAATACAAATGCTTCCAAAATGGGTTC 834
QY 281 PheCysArgSerGluSerProValLeuHisGlnArgGluHisValGluLeuLeuArgGly 300
Db 835 TTCTCCCAATCAGATTCTGTAGCTCTTCCACCAAGGGAACATGTTGAAGCTCTTAGAGCC 894
QY 301 ArgLysLeuAlaArgSerLeuAlaValLeuLeuSerAlaPheAlaIleCysTrpAlaPro 320
Db 895 AGAGATTAGCCCAAGTCACTGCGCATCTCTTAGGGGTTTTTCTGCTGGCTGCCA 954
QY 321 TyrCysLeuPheThrIleValLeuSerThrTyrArgArgGlyGluArgProLysSerIle 340
Db 955 TATTCTCTCTTCCAAATGCTCTTTCATTTTATTCCTCAGCAACAGCTCCTAAATCAGTT 1014
QY 341 TrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerLeuIleAsnProPheLeuTyr 360
Db 1015 TGGTATAGAAATGTCATTTTGGCTTCAGTGGTTCAATTCCTTTGTCAATCTCTTTGTAT 1074
QY 361 ProLeuCysHisArgArgPheGlnLysAlaPheTrpLysIleLeuCysValThrLysGln 380
Db 1075 CCATTTGTGTCAACAGCGCTTCAAGGGCTTTCTTGAANAATATTTTGTATATAAAAGCAA 1134
QY 381 ProAlaProSerGln---ThrGlnSerValSerSer 391
Db 1135 CCTCTACCATCAACACAGTCGGTCAGTATCTTCT 1170

RESULT 12
AAI67750
ID AAI67750 standard; cDNA; 1173 BP.
XX
AC AAI67750;
XX
DT 27-FEB-2002 (first entry)
XX
DE Human histamine H4 receptor protein encoding cDNA.
XX
KW Histamine receptor; H4; antirheumatic; antiarthritic; immunosuppressive;
KW antiasthmatic; antiallergic; neuroprotective; antidiabetic; human;
KW cerebroprotective; cAMP modulator; gene therapy; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
CDS 1..1173
FT /tag= a
FT /product= "histamine H4 receptor"
XX
XX WO200185786-A2.
XX
XX 15-NOV-2001.
XX
XX 04-MAY-2001; 2001WO-US014527.

```

XX 05-MAY-2000; 2000US-0202151P.  
 PR 23-AUG-2000; 2000US-0227567P.  
 PR 13-NOV-2000; 2000US-0247855P.  
 XX  
 XX (AMHP ) AMERICAN HOME PROD CORP.  
 XX  
 PI Jones PG, Blatcher M, Wu S, Pausch MH;  
 XX  
 XX WPI; 2002-049442/06.  
 DR P-PSDB; AAG66023.  
 XX  
 XX New histamine receptor, termed H4 useful for detecting H4 (ant) agonists  
 PT for treating transplanted organ rejection, asthma, allergy, multiple  
 PT sclerosis and rheumatoid arthritis.  
 XX  
 XX Claim 13; Fig 1; 66pp; English.  
 PS  
 CC The invention provides an isolated histamine receptor, H4, which binds  
 CC ligands comprising imidazole attached to amine by an alkyl chain. The H4  
 CC receptor can be expressed by standard recombinant methodology. Cells  
 CC expressing H4 receptor protein at a detectable level can suppress cyclic  
 CC adenosine monophosphate (cAMP) formation when contacted with the H4  
 CC receptor agonist. The H4 receptor and antibodies are used for identifying  
 CC H4 receptor modulators. Modulation of histamine H4 receptors is useful  
 CC for treating transplanted organ rejection, asthma, allergies and  
 CC autoimmune pathologies such as multiple sclerosis, type 1 diabetes,  
 CC rheumatoid arthritis, cognitive and memory defects. The H4 receptor  
 CC protein and nucleic acids are useful targets to identify drugs that are  
 CC effective in treating disorders associated with histamine-regulated  
 CC processes. Identification and isolation of H4 receptor provides for  
 CC development of screening of molecules that interact with H4 receptors.  
 CC Genetic variants of H4 can be used to diagnose an H4 associated disease  
 CC as described above. The H4 receptor polynucleotide is useful to treat or  
 CC prevent a disorder associated with the function of H4 in peripheral blood  
 CC leukocytes. The present sequence represents a cDNA encoding the human  
 CC histamine H4 receptor protein  
 XX  
 SQ Sequence 1173 BP; 296 A; 245 C; 231 G; 401 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 1,37e-119 Length: 1173  
 Score: 1403.50 Matches: 271  
 Percent Similarity: 79.34% Conservative: 40  
 Best Local Similarity: 69.13% Mismatches: 78  
 Query Match: 68.63% Indels: 3  
 DB: 6 Gaps: 2

US-10-626-126-9 (1-391) x AA167750 (1-1173)

QY 1 MetSerGluSerAsnGlyThrAspValLeuProLeuThrAlaGlnValProLeuAlaPhe 20  
 DB 1 ATGCCAGATACATAATAGCACAATCAATTTATCACTAAGCACTCGTGTACTTTAGCATTT 60  
 QY 21 LeuMetSerLeuLeuAlaPheAlaIleThrIleGlyAsnAlaValIleLeuAlaPhe 40  
 DB 61 TTTATGTCTCTAGTAGCTTTTCTATATAGCTAGGAATTCCTTTGTCTATTTAGCTTTT 120  
 QY 41 ValAlaAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60  
 DB 121 GTGGTGGACAAAACCTTAGACATCGAAGTAGTATTTTCTTAACITGGCCATCTCT 180  
 QY 61 AspPhePheValGlyValIleSerIleProLeuTyrIleProHisThrIlePheAsnTrp 80  
 DB 181 GACTTCTTTGTGGGTGTGATCTCCATTCCTTTGTATACATCCCTCACACGCTGTTCGAATGG 240  
 QY 81 AsnProGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrIleLeuCysThrAla 100  
 DB 241 GATTTTGGAAAGAAATCTGTGTAITTTGGCTCACTACTACTACTATCTGTATGTACAGCA 300  
 QY 101 SerValTyrSerIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120  
 DB 301 TCTGTATATAACATTTGCTCTCATCGACTATGATCGATACCTGTCTCAATGCTGTA 360

QY 121 ArgTyrArgAlaGlnHisThrGlyIleLeuIleValAlaGlnMetValAlaValTrp 140  
 DB 361 AGTTATAGAACTCAACATACCTGGGGTCTTGAAGATTGTACTGTGATGGTCCCTTTGG 420  
 QY 141 IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTrpIleAsnSer 160  
 DB 421 GTGCTGGGCTCTTAGTGAATGGGCAATGATTTCTAGTTTCAGAGTCTTGGAGGATGAA 480  
 QY 161 ThrAsnThrGluGluCysGluProGlyPheValThrGluIleTyrIleLeuAlaIleThr 180  
 DB 481 GGTAGT-----GAATGTGAACCTGGATTTTTCGGAATGGTACATCCTTGCCATCACA 534  
 QY 181 AlaPheLeuGluPheLeuProValSerLeuValValTyrPheSerValGlnIleTyr 200  
 DB 535 TCATTTCTTGGAAATTCGTGATCCCATCTATCTAGTCGCTTATTTTCAACATGAATATAT 594  
 QY 201 TrpSerLeuTrpIleAspGlySerLeuSerArgCysProSerHisAlaGlyPheIleAla 220  
 DB 595 TGGACCTGTGGAGCGGTGATCACTCAGTAGGTGCCAAGCCATCCTGGACTGCTGCT 654  
 QY 221 ThrSerSerArgGlyThrGlyHisSerArgArgThrGlyLeuAlaCysArgThrSerLeu 240  
 DB 655 GTCTCTTCCAACTCTGTGGACACTCATTCAGAGGTAGACTATCTTCAAGGAGAGATCTCT 714  
 QY 241 ProGlyLeuIleGluProAlaSerLeuHisSerGluSerProArgGlyIleSerSer 260  
 DB 715 TCTGCATCCAGACAGAGTTCTTCGCACTCTTCATTCAGAGAGACAGAGAGAGAGTAGT 774  
 QY 261 LeuLeuValSerLeuArgThrHisMetSerGlySerIleIleAlaPheIleValGlySer 280  
 DB 775 CTCATGTTTTCTCAAGAACCAAGATGATAGCAATCAATTCCTCCAAATGGGTTC 834  
 QY 281 PheCysArgSerGluSerProValLeuHisGlnArgGluHisValGluLeuLeuArgGly 300  
 DB 835 TTCTCCCAATCAGATTCGTAGCTCTTCCAAAGGGAACATGTTGAACTGCTCAGAGCC 894  
 QY 301 ArgIleLeuAlaArgSerLeuAlaValLeuLeuSerAlaPheAlaIleCysTrpAlaPro 320  
 DB 895 AGGAGATTAGCCAACTGCTGCTCCTCTTAGGGGTTTTTGTCTTGTGGGCTCCA 954  
 QY 321 TyrCysLeuPheThrIleValLeuSerThrTyrArgArgGlyGluArgProIleSerIle 340  
 DB 955 TATTCCTCTGTTTCACTATTTGCTCTTTCATTTTATTCCTCAGCAACAGGCTCTTAATCAGTT 1014  
 QY 341 TrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerLeuIleAsnProPheLeuTyr 360  
 DB 1015 TGGTATAGAAATTCATTTTGGCTTCAGTGGTTTCAATTCCTTTGTCAATCCTCTTTTGTAT 1074  
 QY 361 ProLeuCysHisArgArgPheGlnIleValAlaPheTrpIleLeuCysValThrIleGln 380  
 DB 1075 CCATTTGTGTCAACAGCGCTTTCAAAGGCTTTCTTGAATAATATTTTGTATATAAAGCAA 1134  
 QY 381 ProAlaProSerGln---ThrGlnSerValSerSer 391  
 DB 1135 CCTCTACCATCAACACAGCTGGTCACTATCTTCT 1170  
 RESULT 13  
 ID ACA93262  
 XX ACA93262 standard; cDNA; 1173 BP.  
 AC ACA93262;  
 XX  
 DT 16-JUL-2003 (first entry)  
 DE Human cDNA encoding GPCR hRUP7.  
 KW  
 KW Human; ss: gene; orphan G protein-coupled receptor; GPCR; hARE-3; hARE-4;  
 KW hARE-5; hRUP3; hRUP5; hRUP6; hRUP7; hGPCR27; hARE-1; hARE-2; hPPR1; hG2A;  
 KW hCHN3; hCHN4; hCHN6; hCHN8; hCHN9; hCHN10; hRUF4; signalling cascade.  
 OS Homo sapiens.  
 XX

```

PN US2003017528-A1.
XX
PD 23-JAN-2003.
XX
PF 06-JUN-2001; 2001US-00875076.
XX
PR 20-NOV-1998; 98US-0109213P.
PR 16-FEB-1999; 99US-0120416P.
PR 26-FEB-1999; 99US-0121852P.
PR 12-MAR-1999; 99US-0123946P.
PR 12-MAR-1999; 99US-0123946P.
PR 28-MAY-1999; 99US-0123949P.
PR 28-MAY-1999; 99US-0136436P.
PR 28-MAY-1999; 99US-0136437P.
PR 28-MAY-1999; 99US-0136439P.
PR 28-MAY-1999; 99US-0136567P.
PR 28-MAY-1999; 99US-0137127P.
PR 28-MAY-1999; 99US-0137131P.
PR 29-JUN-1999; 99US-0141448P.
PR 28-SEP-1999; 99US-0156333P.
PR 29-SEP-1999; 99US-0156555P.
PR 29-SEP-1999; 99US-0156634P.
PR 12-OCT-1999; 99US-00417044.
XX
XX (CHEN/) CHEN R.
XX (DANG/) DANG H T.
XX (LIAN/) LIAN C W.
XX (LINI/) LIN I.
XX
Chen R, Dang HT, Liaw CW, Lin I;
XX
XX WPI; 2003-428952/40.
XX P-PSDB; ABU92265.
XX
Novel endogenous, orphan, human G protein-coupled receptors useful for
identification of modulators of the receptor and as research tools for
understanding the role of the receptor in human body.
XX
PS Claim 25; Page 22; 54pp; English.
XX
The invention relates to a human G protein-coupled receptor (GPCR)
appearing as ABU92259-ABU92277 (encoded by cDNAs ACA93256-ACA93274) named
HARE-3, HARE-4, HARE-5, HRUP3, HRUP5, HRUP6, HRUP7, hGCR27, HARE-1, HARE
-2, hPPR1, hG2A, hCHN8, hCHN4, hCHN6, hCHN9, hCHN10 and hRUF4.
XX Also included are a plasmid comprising a vector and one of the cDNAs
above and a host cell comprising the plasmid. The GPCRs are useful for
the direct identification of candidate compounds as inverse agonists,
agonists or partial agonists. In vitro and in vivo systems incorporating
GPCRs are useful for elucidating and understanding the roles these
receptors play in the human condition, both normal and diseased, as well
as understanding the role of constitutive activation as it applies to
understanding the signalling cascade. The cDNAs are useful for making a
probe for dot-blot analysis against tissue mRNA and/or RT-PCR
XX identification of the expression of the receptor in tissue samples. The
present sequence is a cDNA encoding a GPCR of the invention
XX
SQ Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;
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Pred. No.: 1-37e-119 Length: 1173
Score: 1403.50 Matches: 271
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US-10-626-126-9 (1-391) x ACA93262 (1-1173)
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ID ADG98759 standard; cDNA; 1173 BP.

XX AC ADG98759;  
XX 11-MAR-2004 (first entry)  
XX Human orphan GPCR cDNA, RUP7.  
XX Human; G protein-coupled receptor; GPCR; research tool; gene; ss.  
XX Homo sapiens.  
XX Key Location/Qualifiers  
XX CDS 1..1173  
XX FT /\*tag= a  
XX FT /product= "Human GPCR protein"

XX US2003148450-A1.

XX 07-AUG-2003.

XX 17-OCT-2002; 2002US-00272983.

XX 20-NOV-1998; 98US-01092113P.

XX 16-FEB-1999; 99US-0120416P.

XX 26-FEB-1999; 99US-0121852P.

XX 12-MAR-1999; 99US-0123946P.

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XX 28-MAY-1999; 99US-0136436P.

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XX 28-MAY-1999; 99US-0136567P.

XX 28-MAY-1999; 99US-0137127P.

XX 28-MAY-1999; 99US-0137131P.

XX 29-JUN-1999; 99US-0141448P.

XX 28-SEP-1999; 99US-0156333P.

XX 29-SEP-1999; 99US-0156555P.

XX 29-SEP-1999; 99US-0156634P.

XX 12-OCT-1999; 99US-00417044.

XX (CHEN/) CHEN R.

XX (DANG/) DANG H T.

XX (LIAN/) LIAN C W.

XX (LINI/) LIN I.

XX Chen R, Dang HT, Lian CW, Lin I;

XX WPI: 2003-897571/82.

XX P-PSDB; ADG98760.

XX New cDNA encoding a human G protein coupled receptor, useful for making a probe for dot-blot analysis against tissue-mRNA, and/or for RT-PCR identification of the expression of the receptor in tissue samples.

XX Claim 25; SEQ ID NO 13; 52pp; English.

XX The present invention provides novel human G protein-coupled receptor (GPCR) proteins and their encoding nucleic acids. The invention is useful for making a probe for dot-blot analysis and for RT-PCR identification of the expression of the receptor in tissue samples. The invention is also useful for identifying candidate compounds as inverse agonists, agonists or partial agonists and as research tools in determining the location of the receptors within the body. The present sequence is human orphan G protein-coupled receptor cDNA.

XX Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;

Percent Similarity: 79.34% Conservative: 40  
Best Local Similarity: 69.13% Mismatches: 78  
Query Match: 68.63% Indels: 3  
DB: 10 Gaps: 2

US-10-626-126-9 (1-391) x ADG98759 (1-1173)

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DB	61	TTTATGTCCTTAGTACTTTTGTATATATGCTAGGAATGCTTGTGTCATTTAGCTTTT	120
QY	41	ValAlaAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer	60
DB	121	GTGGTGGACAAAACCTTAGACATCGAAGTAGTATTATTTTCTTAACCTTGCCATCTCT	180
QY	61	AspPhePheValGlyValIleSerIleProLeuTyrIleProHisThrLeuPheAsnTyr	80
DB	181	GACTTCCTTTGGGGTGTGATCTCCATTCCTTTGTACATCCCTCACCGCTGTGCAATGG	240
QY	81	AsnProGlySerGlyIleCysMetPheTyrLeuIleThrAspTyrLeuLeuCysThrAla	100
DB	241	GATTTTGGAAAGGAATCTGTGTTATTTGGCTCACTACTGACTATCTGTTATGTACGCA	300
QY	101	SerValTyrSerIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal	120
DB	301	TCTGTATATAACATTTGCTCATCAGCTATGATCATCAGCTCTGCTGCTCAATGCTGTG	360
QY	121	ArgTyrArgAlaGlnHisThrGlyIleLeuIleValAlaGlnMetValAlaValTyr	140
DB	361	TCTTATAGAACTCAACATCTGGGCTCTGAAGATTTGTTCTCTGATGGTGGCCGTTTGG	420
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QY	161	ThrAsnThrGluGluCysGluProGlyPheValThrGluTyrTyrIleLeuAlaIleThr	180
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QY	221	ThrSerSerArgGlyThrGlyHisSerArgArgThrGlyLeuAlaCysArgThrSerLeu	240
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QY	241	ProGlyLeuLysGluProAlaAlaSerLeuHisSerGluSerProArgGlyLysSerSer	260
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QY	261	LeuLeuValSerLeuArgThrHisMetSerGlySerIleIleAlaPheLysValGlySer	280
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DB	835	TTCTCCCAATCAGATTTGTAGCTCTTCCAAAGGGAACATGTTGAATGCTGTAGAGCC	894
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Alignment Scores:  
Pred. No.: 1.37e-119 Length: 1173  
Score: 1403.50 Matches:









GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: August 5, 2005, 14:55:30 ; Search time 702 Seconds  
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Total number of hits satisfying chosen parameters: 14594722

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a

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SUMMARIES

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2	2034	99.5	1176	21	US-10-626-126-6 Sequence 6, Appli
3	2034	99.5	1176	21	US-10-626-398-6 Sequence 6, Appli
4	1742	85.2	1176	21	US-10-626-445-5 Sequence 5, Appli
5	1742	85.2	1176	21	US-10-626-126-5 Sequence 5, Appli
6	1742	85.2	1176	21	US-10-626-398-5 Sequence 5, Appli
7	1403.5	68.6	1173	9	US-09-812-216-1 Sequence 1, Appli
8	1403.5	68.6	1173	9	US-09-910-411-1 Sequence 1, Appli
9	1403.5	68.6	1173	10	US-09-875-076-13 Sequence 13, Appl
10	1403.5	68.6	1173	10	US-09-876-252-13 Sequence 13, Appl
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12	1403.5	68.6	1173	15	US-10-272-983-13 Sequence 13, Appl
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14	1403.5	68.6	1173	16	US-10-393-807-13 Sequence 13, Appl
15	1403.5	68.6	1173	17	US-10-417-820A-13 Sequence 13, Appl
16	1403.5	68.6	1173	18	US-10-349-253A-1 Sequence 13, Appl
17	1403.5	68.6	1173	19	US-10-723-955-13 Sequence 13, Appl
18	1403.5	68.6	1173	19	US-10-782-596-13 Sequence 13, Appl
19	1403.5	68.6	1173	19	US-10-737-619-1 Sequence 1, Appli
20	1403.5	68.6	1173	20	US-10-626-445-1 Sequence 1, Appli
21	1403.5	68.6	1173	21	US-10-616-088-1 Sequence 1, Appli
22	1403.5	68.6	1173	21	US-10-626-126-1 Sequence 1, Appli
23	1403.5	68.6	1173	21	US-10-626-398-1 Sequence 1, Appli
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28	1403.5	68.6	3889	21	US-10-684-206-19 Sequence 19, Appl
29	1398.5	68.4	1173	15	US-10-290-078-26 Sequence 26, Appl
30	1398.5	68.4	1265	15	US-10-290-078-25 Sequence 25, Appl
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38	693	33.9	1335	19	US-10-727-021-6 Sequence 6, Appli
39	693	33.9	2050	9	US-09-891-053-21 Sequence 21, Appl
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ALIGNMENTS

RESULT 1  
US-10-626-445-6  
; Sequence 6, Application US/10626445  
; Publication No. US20040248252A1  
; GENERAL INFORMATION:  
; APPLICANT: Lovenberg, Timothy  
; APPLICANT: Liu, Changlu  
; TITLE OF INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Subtype  
; FILE REFERENCE: PRD-0032  
; CURRENT APPLICATION NUMBER: US/10/626,445  
; PRIOR FILING DATE: 2003-07-23  
; PRIOR APPLICATION NUMBER: 09/790,849  
; PRIOR FILING DATE: 2001-02-22  
; PRIOR APPLICATION NUMBER: 60/208,260  
; PRIOR FILING DATE: 2000-05-31  
; NUMBER OF SEQ ID NOS: 27

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/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 6
/ LENGTH: 1176
/ TYPE: DNA
/ ORGANISM: Rattus rattus
US-10-626-445-6

Alignment Scores:
Pred. No.: 4,28e-215 Length: 1176
Score: 2034.00 Matches: 390
Percent Similarity: 99.74% Conservative: 0
Best Local Similarity: 99.74% Mismatches: 1
Query Match: 99.46% Indels: 0
DB: 20 Gaps: 0

US-10-626-126-9 (1-391) x US-10-626-445-6 (1-1176)

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Qy 21 LeuMetSerLeuLeuAlaPheAlaIleThrIleGlyAsnAlaValIleLeuAlaPhe 40
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Qy 41 ValAlaAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60
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Qy 81 AsnProGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrIleuLeuCysThrAla 100
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RESULT 2
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; Sequence 6, Application US/10626126
; Publication No. US20050074770A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Changlu
; TITLE OF INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Subtype
; FILE REFERENCE: PRD-0033
; CURRENT APPLICATION NUMBER: US/10/626,126
; PRIOR FILING DATE: 2003-07-23
; PRIOR APPLICATION NUMBER: 09/790,849
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/208,260
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 1176
; TYPE: DNA
; ORGANISM: Rattus rattus
US-10-626-126-6

Alignment Scores:
Pred. No.: 4,28e-215 Length: 1176
Score: 2034.00 Matches: 390
Percent Similarity: 99.74% Conservative: 0
Best Local Similarity: 99.74% Mismatches: 1
Query Match: 99.46% Indels: 0
DB: 21 Gaps: 0

US-10-626-126-9 (1-391) x US-10-626-126-6 (1-1176)

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QY 301  ArgLysLeuAlaArgSerLeuAlaValLeuLeuSerAlaPheAlaIleCysTrpAlaPro 320
Db 901  AGGAAGTAGCAGGTGCTAGTGTCTCTCCTGAGTGTCTTGGCATTGCTGGGCTCG 960

QY 321  TyrCysLeuPheThrIleValLeuSerThrTyrArgArgGlyGluArgProLysSerIle 340
Db 961  TATTGGCTGTTCACAAATTTGTTCTTCAACTTATCGCAGAGGGAGCGGCCCAAAATCGATT 1020

QY 341  TrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerLeuIleAsnProPheLeuTyr 360
Db 1021  TGGTACAGCATAGCCTTTGGCTACAGTGGTGTCAATTCATTAATCCCTTTCTATAC 1080

QY 361  ProLeuCysHisArgArgPheGlnLysAlaPheTrpLysIleLeuCysValThrLysGln 380
Db 1081  CCTTTGTGCCACAGACGTTTCCAGAGGCTTTCTGGAGAGATCTCTGTGTGACAAAGCAA 1140

QY 381  ProAlaProSerGlnThrGlnSerValSerSer 391
Db 1141  CCAGCACCTTCCAGACCCAGTCAGTATCTTCT 1173

```

RESULT 3

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US-10-626-398-6
; Sequence 6, Application US/10626398
; Publication No. US20050074841A1
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Liu, Changlu
; TITLE OF INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Subtype
; FILE REFERENCE: PRD-0034

```

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; CURRENT APPLICATION NUMBER: US/10/626,398
; CURRENT FILING DATE: 2003-07-23
; PRIOR APPLICATION NUMBER: 09/790,849
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/208,260
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 1176
; TYPE: DNA
; ORGANISM: Rattus rattus
; US-10-626-398-6

Alignment Scores:
Pred. No.: 4,28e-215 Length: 1176
Score: 2034.00 Matches: 390
Percent Similarity: 99.74% Conservative: 0
Best Local Similarity: 99.74% Mismatches: 1
Query Match: 99.46% Indels: 0
DB: 21 Gaps: 0

US-10-626-126-9 (1-391) x US-10-626-398-6 (1-1176)

QY 1  MetSerGluSerAsnGlyThrAspValLeuProLeuThrAlaGlnValProLeuAlaPhe 20
Db 1  ATGTCCGAGCTTAACGGCCTGACGCTTTGCCACTGCTCAAGTCCCTTTGGCATTT 60

QY 21  LeuMetSerLeuLeuAlaPheAlaIleThrIleGlyAsnAlaValValIleLeuAlaPhe 40
Db 61  TTAATGTCCTGCTTCTTCTTGTATTAACGATAGGCAATGCTGTGTCAITTTAGCCTTT 120

QY 41  ValAlaAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60
Db 121  GTAGCAGACAGAAACCTTAGACATCGAAGTAATATTTTCTTAATTTGGCTATTTCT 180

QY 61  AspPhePheValGlyValIleSerIleProLeuTyrIleProHisThrLeuPheAsnTrp 80
Db 181  GACTTCTTCGTGGGTGTCATCTCCATTCCTCTGTACATCCCTCACACGCTGTTTAACTGG 240

QY 81  AsnProGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeuLeuCysThrAla 100
Db 241  AATTTGGGAAGTGGAACTGCGATGTTTGGCTCATTAAGTACATCTTTTGTGCACAGCA 300

QY 101  SerValTyrSerIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120
Db 301  TCGGTCTACAGATTGTTCTCATTAAGTACGATCGATACGATCAGTTTCAAAAGCTGTG 360

QY 121  ArgTyrArgAlaGlnHisThrGlyIleLeuLeuIleValAlaGlnMetValAlaValTrp 140
Db 361  CGTTATAGACACAGCACACTGCGATCCTGAAATTTGCTCAAAATGGTGGCTGTTGG 420

QY 141  IleLeuAlaPheLeuValLeuValLeuGlyProMetIleLeuAlaSerAspSerTrpLysAsnSer 160
Db 421  ATACTGGCTTTCTTGTGTCAATGGCCCAATGATTCGTGGCTTCGGATTTCTTGGAAAGACAG 480

QY 161  ThrAsnThrGluGluCysGluProGlyPheValThrGluTrpTyrIleLeuAlaIleThr 180
Db 481  ACCAACACAGAGAGTGGAGTCTCAGTAGTGCCCTAGCCAGCTGTGATTCATCGCT 540

QY 181  AlaPheLeuGluPheLeuLeuProValSerLeuValValTyrPheSerValGlnIleTyr 200
Db 541  GCATTTCTGGAAATTCCTGCTCCCTGCTCTCTGCTGCTATTTTCAAGTGTACAGATTAC 600

QY 201  TrpSerLeuTrpLysArgGlySerLeuSerLeuValValTyrPheSerValGlnIleTyr 220
Db 601  TGGAGCTGTGGAAAGCGTGGAGTCTCAGTAGTGCCCTAGCCAGCTGTGATTCATCGCT 660

QY 221  ThrSerSerArgGlyThrGlyHisSerArgArgThrGlyLeuAlaCysArgThrSerLeu 240
Db 661  ACCTCTTCCAGGGGCACTGGACACTCAGCAGAACTGGGTGGCTTGTAGCAAGTCTT 720

QY 241  ProGlyLeuLysGluProAlaIleSerLeuHisSerGluSerProArgGlyLysSerSer 260

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Db 721 CCTGGATTAAAGAACACAGCGCATCCCTTCATTAGAAAGTCCACGAGAAAGAGCAGT 780
Qy 261 LeuLeuValSerLeuArgThrHisMetSerGlySerIleAlaPheLysValGlySer 280
Db 781 CTCCTGGTGTCTTAAAGACTCACATGAGCGTAGTATCATCGCCTTCAAAGTGGGTTC 840
Qy 281 PheCysArgSerGlySerProValLeuHisGlnArgGluHisValGluLeuLeuArgGly 300
Db 841 TTCCTCCGATCAGAAGCCAGTGTCTTCCAGAGAGACGACGTGAGGCTTCTCAGAGC 900
Qy 301 ArgLysLeuAlaArgSerLeuAlaValLeuLeuSerAlaPheAlaIleCysTrpAlaPro 320
Db 901 AGGAAGCTAGCCAGGTGCTGCTCCTCTGAGTGTCTTTGGCCATTGTCTGGGCTCG 960
Qy 321 TyrCysLeuPheThrIleValLeuSerThrTyrArgArgGlyGluArgProLysSerIle 340
Db 961 TATTGCTGTTCACAAATGTTCTTTCACTTATCGCAGAGGGAGCGGCCCAATCGATT 1020
Qy 341 TrpTyrSerIleAlaPheThrLeuGlnTrpPheAsnSerLeuIleAsnProPheLeuTyr 360
Db 1021 TGGTACAGCATAGCCTTTGGCTACAGTGTTCATTTCAATTCATTATTAATCCCTTTCTATAC 1080
Qy 361 ProLeuCysHisArgArgPheGlnLysAlaPheThrLysIleLeuCysValThrLysGln 380
Db 1081 CCTTTGTGCCACAGAGTTCAGAAAGGCTTTCTGGAAGATACTCTGTGTGACAAAGCAA 1140
Qy 381 ProAlaProSerGlnThrGlnSerValSerSer 391
Db 1141 CCAGCACCTTCACAGACCCAGTCAGTATCTTCT 1173

RESULT 4
US-10-626-445-5
; Sequence 5, Application US/10626445
; Publication NO. US20040248252A1
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Liu, Changliu
; TITLE OF INVENTION: DNA Encoding Mammalian Histamine Receptor Of The H4 Subtype
; FILE REFERENCE: PRD-0032
; CURRENT APPLICATION NUMBER: US/10/626,445
; CURRENT FILING DATE: 2003-07-23
; PRIOR APPLICATION NUMBER: 09/790,849
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/208,260
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 1176
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-626-445-5

Alignment Scores:
Pred. No.: 1,12e-182 Length: 1176
Score: 1742.00 Matches: 332
Percent Similarity: 89.26% Conservatives: 17
Best Local Similarity: 84.91% Mismatches: 42
Query Match: 85.18% Indels: 0
DB: 20 Gaps: 0

US-10-626-126-9 (1-391) x US-10-626-445-5 (1-1176)
Qy 1 MetSerGluSerAsnGlyThrAspValLeuLeuProLeuThrAlaGlnValProLeuAlaPhe 20
Db 1 ATGTCCGAGCTAAACAGTACTGGCATCTTGGCACCAGCTGCTCAGGTCCCTTGGCATTT 60
Qy 21 LeuMetSerLeuLeuAlaPheAlaIleThrIleGlyAsnAlaValIleLeuAlaPhe 40
Db 61 TTAATGCTTCATTTGCCCTTGTCTATATAGTGGCAATGCTGTGTGTCATCTTAGCCTTT 120
Qy 41 ValAlaAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60
Db 121 GTGGTGGACAGAACCTTAGACATCGAAGTAATATATTTTCTTAAATTTGGCTATTCT 180
Qy 61 AspPhePheValGlyValIleSerIleProLeuTyrIleProHisThrLeuPheAsnTrp 80
Db 181 GACTTCTCTGGTGGTTCGATTTCCTGTATACATCCCTCAGCTGTGTAACTGG 240
Qy 81 AsnProGlySerGlyCysMetPheTrpLeuIleThrAspTyrLeuLeuCysThrAla 100
Db 241 AATTTTGAAGTGAATCTGCATGTTTGGCTCATCTACTGACTATCTTTTGTGACCCGA 300
Qy 101 SerValTyrSerIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120
Db 301 TCTGTCTACAATATGTCTCTCATTAGCTACGATCGATACCATCAGTCAAGTTCAAATGCTGTG 360
Qy 121 ArgTyrArgAlaGlnHisThrGlyIleLeuLysIleValAlaGlnMetValAlaValTrp 140
Db 361 TCTTATAGGGCTCAACACATGGCATCATGAAGATTGTGTCTCAATGGTGGCTGTGTGG 420
Qy 141 IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTrpLysAsnSer 160
Db 421 ATACTGGCTTCTCTGTAAATGGCCCGATGATTCCTGGCTTCAGATTCTTTGGAAGAACAC 480
Qy 161 ThrAsnThrGluGluCysGluProGlyPheValThrGluTrpTyrIleLeuAlaIleThr 180
Db 481 ACGAACACAAAGGACTGTGAGCTGGCTTGTTCAGAGTGGTACATCTCCACCATTTACA 540
Qy 181 AlaPheLeuGluPheLeuLeuProValSerLeuValValTyrPheSerValGlnIleTyr 200
Db 541 ATGCTCTTTGGAATTCCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 600
Qy 201 TrpSerLeuTrpLysArgGlySerLeuSerArgCysProSerHisAlaGlyPheIleAla 220
Db 601 TGGAGCCTGTGAAGCGTAGGCTCTCAGTAGTGCCCTTAGCCATGCTGGATTCTCCACT 660
Qy 221 ThrSerSerArgGlyThrGlyHisSerArgArgThrGlyLeuAlaCysArgThrSerLeu 240
Db 661 ACCTCTCCAGCTTCAGGACCTTACACAGAGCTGGGTGGCTTGCAGGACAAAGTAAT 720
Qy 241 ProGlyLeuLysGluProAlaAlaSerLeuHisSerGluSerProArgGlyLysSerSer 260
Db 721 CCTGGATTGAAGGAATCAGCTGCTCTGCTCACTCAGAAAGTCTCTCGAAGAAAGAGCAG 780
Qy 261 LeuLeuValSerLeuArgThrHisMetSerGlySerIleIleAlaPheLysValGlySer 280
Db 781 ATCCTGGTGTCTTAAAGACTCACATGAACAGCAGTATCATCTGCTTCAAAGTGGGTTC 840
Qy 281 PheCysArgSerGluSerProValLeuHisGlnArgGluHisValGluLeuLeuArgGly 300
Db 841 TTCCTCCGATCAGAAGTGCAGCGCTTCGCCAAAGGAGTACGACAGCTTCTCAGAGC 900
Qy 301 ArgLysLeuAlaArgSerLeuAlaValLeuLeuSerAlaPheAlaIleCysTrpAlaPro 320
Db 901 AGGAAGCTAGCCAGGTGCTGCTCCTCTGAGTGTCTTTGGCCATTGTCTGGGCTCG 960
Qy 321 TyrCysLeuPheThrIleValLeuSerThrTyrArgArgGlyGluArgProLysSerIle 340
Db 961 TACTGTCTGTTCACAAATGTTCTTCACTTACCAGAACCGAACGCCCAATCCGGTG 1020
Qy 341 TrpTyrSerIleAlaPheThrLeuGlnTrpPheAsnSerLeuIleAsnProPheLeuTyr 360
Db 1021 TGGTACAGCATTTGCCCTTCTGGCTGCAATGGTTCAATTCGTTTAAATCCCTTTCTGTAC 1080
Qy 361 ProLeuCysHisArgArgPheGlnLysAlaPheThrLysIleLeuCysValThrLysGln 380
Db 1081 CCTTTGTGTACAGCGTTCAGAAAGGCTTTCTGGAAGATACTTTGTGTGACAAAGCAA 1140
Qy 381 ProAlaProSerGlnThrGlnSerValSerSer 391
Db 1141 CCAGCGCTGTCAAGAACCCAGTCAGTATCTTCT 1173

RESULT 5
US-10-626-126-5
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; Sequence 5, Application US/10626126  
 ; Publication No. US20050074770A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Lovenberg, Timothy  
 ; APPLICANT: Liu, Changlu  
 ; TITLE OF INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Subtype  
 ; FILE REFERENCE: PRD-0033  
 ; CURRENT APPLICATION NUMBER: US/10/626,126  
 ; CURRENT FILING DATE: 2003-07-23  
 ; PRIOR APPLICATION NUMBER: 09/790,849  
 ; PRIOR FILING DATE: 2001-02-22  
 ; PRIOR APPLICATION NUMBER: 60/208,260  
 ; PRIOR FILING DATE: 2000-05-31  
 ; NUMBER OF SEQ ID NOS: 27  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 5  
 ; LENGTH: 1176  
 ; TYPE: DNA  
 ; ORGANISM: Mus musculus  
 US-10-626-126-5

Alignment Scores:  
 Pred. No.: 1,12e-182 Length: 1176  
 Score: 1742.00 Matches: 332  
 Percent Similarity: 89.26% Conservativeness: 17  
 Best Local Similarity: 84.91% Mismatches: 42  
 Query Match: 85.18% Indels: 0  
 DB: 21 Gaps: 0

US-10-626-126-9 (1-391) x US-10-626-126-5 (1-1176)

Qy	1	MetSerGluSerAsnGlyThrAspValLeuProLeuThrAlaGlnValProLeuAlaPhe	20
Db	1	ATGTCGGAGTCTAACAGTACTGGCATCTTGCCACCAGCTGCTCAGGTCCCTTGGCATTT	60
Qy	21	LeuMetSerLeuAlaPheAlaIleThrIleGlyAsnAlaValIleLeuAlaPhe	40
Db	61	TTAATGCTCTTCAATTTGGCTTTGCTATAATGGTAGGTAATGCTGTGGTTCATCTTAGCCCTTT	120
Qy	41	ValAlaAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer	60
Db	121	GTGGTCGACAGAAACCTTAGACATCGAAGTAATATTTTTTCTTAATTTGGCTATTCT	180
Qy	61	AspPhePheValGlyValIleSerIleProLeuTyrIleProHisThrLeuPheAsnTrp	80
Db	181	GACTTCCTCGTGGTTTGATTTCCATCTCTGTATACATCCCTCAGCTGTGTGTTAACTGG	240
Qy	81	AsnProGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeuLeuCysThrAla	100
Db	241	AATTTTGGAGTGGAAATCTGCATGTTTGGCTCATTTACTGACTATCTTTTGTGACGCGCA	300
Qy	101	SerValTyrSerIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal	120
Db	301	TCGTCTCAAAATTTGCTCTATTAGTACGATCATGATCCAGTTCAGATTTCAAAATGCTGTG	360
Qy	121	ArgTyrArgAlaGlnHisThrGlyIleLeuIleValAlaGlnMetValAlaValTrp	140
Db	361	TCATTAGGGCTCAACACTGGCATCATGAGATTTGTCTCAAAATGGTGGCTTTGG	420
Qy	141	IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTrpLysAsnSer	160
Db	421	ATACTGGCTTTCTTGGTAAATGGCCGATGATTTCTGGCTTCAGATTTCTGGAAGACAGC	480
Qy	161	ThrAsnThrGluGluCysGluProGlyPheValThrGluTrpTyrIleLeuAlaIleThr	180
Db	481	ACGAACACAAAGACAGTGTGAGCTGCTTTGTGTACAGATGGTATCATCTCACCATTACA	540
Qy	181	AlaPheLeuGluPheLeuLeuProValSerLeuValTyrPheSerValGlnIleTyr	200
Db	541	ATGCTCTTGGAAATCTCTGCTCATCTCTGGCTTATTTTCAATGTACAGATTAC	600
Qy	201	TrpSerLeuTrpLysArgGlySerLeuSerArgCysProSerHisAlaGlyPheIleAla	220

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Db 1 ATGTCGAGCTCAACAGTACTGGCATCTTGGCCACAGCTGCTCAGGTCCCTTGGCATTT 60
Qy 21 LeuMetSerLeuLeuAlaPheAlaIleThrIleGlyAsnAlaValIleLeuAlaPhe 40
Db 61 TTAAATGCTTCATTTGCCCTTTCCTATAATGGTAGGCAATGCTGTGGTCACTATGACCTTT 120
Qy 41 ValAlaAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60
Db 121 GTGGTGGACAGAACTTAGACATCGAAGTAATATTTTTTTCTTAATTTGGCTATTTCT 180
Qy 61 AspPhePheValGlyValIleSerIleProLeuTyrIleProHisThrLeuPheAsnTyr 80
Db 181 GACTTCCCTCGTGGGTTCATTTCCATTCCTGTACATCCCTCACGTGTGTGTTAACTGG 240
Qy 81 AsnProGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeuLeuCysThrAla 100
Db 241 AATTTTGGGAAGTGAATCTGCATGTTTGGCTCATTTACTGACTATCTTTTGTGCAACGCA 300
Qy 101 SerValTyrSerIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120
Db 301 TCTGTCTCAATATTTGCTCTATTAGTACGATCGATACAGTTCAGTTTCAAAATGCTGTG 360
Qy 121 ArgTyrArgAlaGlnHisThrGlyIleLeuLysIleValAlaGlnMetValAlaValTyr 140
Db 361 TCTTATAGGCTCAACACACTGAGTGGGTCTTGAAGATTGTTACTCTGATGGCGCTTGG 420
Qy 141 IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTrpLysAsnSer 160
Db 421 ATACTGGCTTTCTTGGTAATGCCCGATGATTTCTGGCTTCAGATTCTTTGGGAAGACAGC 480
Qy 161 ThrAsnThrGluGluCysGluProGlyPheValThrGluTyrTrpIleLeuAlaIleThr 180
Db 481 AGAACACAAAGGACTGTGAGCTGGCTTGTTCACAGAGTGTACATCTCCACATTACA 540
Qy 181 AlaPheLeuGluPheLeuLeuProValSerLeuValValTyrPheSerValGlnIleTyr 200
Db 541 ATGCTCTTGGAAATCTCTGCTTCTGTCACTCTGTGGCTTATTTCAATGTACAGATTTAC 600
Qy 201 TrpSerLeuTyrIleValArgGlySerLeuSerArgCysProSerHisAlaGlyPheIleAla 220
Db 601 TGGAGCCTGTGGAAGCTTAGGGCTCTCAGTAGGTGCCCTAGCCATGCTGGATTCTCCACT 660
Qy 221 ThrSerSerArgGlyThrGlyHisSerArgArgThrGlyLeuAlaCysArgThrSerLeu 240
Db 661 ACCTCTTCAGTGCTTCAGACACTTACACAGACTGGGTGGCTTGCAGGACAGTAAT 720
Qy 241 ProGlyLeuLysGluProAlaAlaSerLeuHisSerGluSerProArgGlyLysSerSer 260
Db 721 CCTGGATTGAAGGAATCAGCTGCATCTCGTCACTCAGAAAGTCTCGAAAGAAAGACAGC 780
Qy 261 LeuLeuValSerLeuArgThrHisMetSerGlySerIleIleAlaPheLysValGlySer 280
Db 781 ATCTCTGGTGTCTTAAGGACTCACATGAACAGCAGTATCATCGCTTCAAAAGTGGGTGCC 840
Qy 281 PheCysArgSerGluSerProValLeuHisGlnArgGluHisValGluLeuLeuArgGly 300
Db 841 TTCTGGCGATCGGAAGTGCAGCGCTTCGCCAAAGGAGTAGCAGAGCTTTCAGAGGC 900
Qy 301 ArgLysLeuAlaArgSerLeuAlaValLeuLeuSerAlaPheAlaIleCysTrpAlaPro 320
Db 901 AGGAAGCTAGCCAGGCTCACTGGCCATCTCTGAGCGCTTTTGCCATTTGCTGGGCTCCA 960
Qy 321 TyrCysLeuPheThrIleValLeuSerThrTyrArgArgGlyGluArgProLysSerIle 340
Db 961 TACTGTCTGTTTCACAATTTGCTTTCACTTACCCAGAACAGCAGCCCAAAATGGGTG 1020
Qy 341 TrpTyrSerIleAlaPheTrpLeuGlnTyrPheAsnSerLeuIleAsnProPheLeuTyr 360
Db 1021 TGGTACAGCATTTGCCCTCTGGCTGCAATGGTTCAATTCCTTTGTTAAATCCCTTCTGTAC 1080
Qy 361 ProLeuCysHisArgArgPheGlnLysAlaPheTrpLysIleLeuCysValThrLysGln 380
Db 1081 CCTTTGTGTACAGGGCTTTCCAGAAGGCTTTCTGGAAGATACCTTTGTGTGCAAAAGCAA 1140
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Qy 381 ProAlaProSerGlnThrGlnSerValSerSer 391
Db 1141 CCAGCGCTGTACAGAACCAAGTCAGTATCTTCT 1173
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## RESULT 7

US-09-812-216-1

; Sequence 1, Application US/09812216

; Patent No. US20020098539A1

; GENERAL INFORMATION:

; APPLICANT: Behan, Jiang Xu

; APPLICANT: Hedrick, Joseph A.

; APPLICANT: Laz, Thomas M.

; APPLICANT: Monsma, Frederick J. Jr.

; APPLICANT: Morse, Kelley L.

; APPLICANT: Umland, Shelby P.

; APPLICANT: Wang, Suke

; TITLE OF INVENTION: Histamine receptor

; FILE REFERENCE: CN01069

; CURRENT APPLICATION NUMBER: US/09/812,216

; CURRENT FILING DATE: 2001-03-19

; PRIOR APPLICATION NUMBER: 09/414,010

; NUMBER OF SEQ ID NOS: 8

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 1

; LENGTH: 1173

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-812-216-1

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Alignment Scores:
Pred. No.: 4,25e-145 Length: 1173
Score: 1403.50 Matches: 271
Percent Similarity: 79.34% Conservative: 40
Best Local Similarity: 69.13% Mismatches: 78
Query Match: 68.63% Indels: 3
DB: 9 Gaps: 2
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US-10-626-126-9 (1-391) x US-09-812-216-1 (1-1173)

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Qy 1 MetSerGluSerAsnGlyThrAspValLeuProLeuThrAlaGlnValProLeuAlaPhe 20
Db 1 ATGCCAGATACATAAGCACAAATCAATTTATCACTAAGCACTCGTGTACTTTAGCATTT 60
Qy 21 LeuMetSerLeuLeuAlaPheAlaIleThrIleGlyAsnAlaValIleLeuAlaPhe 40
Db 61 TTTATGTCTTAGTAGCTTTTGTCTATAATGCTAGGAAATGCTTTGTCATTTTAGCTTTT 120
Qy 41 ValAlaAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60
Db 121 GTGGTGGACAAACCTTAGACATCGAAGTAGTATTTTTTTCTTAACCTGGCCATCTCT 180
Qy 61 AspPhePheValGlyValIleSerIleProLeuTyrIleProHisThrLeuPheAsnTyr 80
Db 181 GACTTCTTTGTGGGTGTGATCTCCATTCCTTTGTATACATCCCTCACAGCTGTTGGAATGG 240
Qy 81 AsnProGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeuLeuCysThrAla 100
Db 241 GATTTTGGAAAGCAAACTGTGTATTTTGGCTCACTACTGACTATCTGTATGTATGACAGA 300
Qy 101 SerValTyrSerIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120
Db 301 TCTGTATATAACATGCTCTCATCAGCATGATGATCATCTGCTAGTCTCAATATGCTGTG 360
Qy 121 ArgTyrArgAlaGlnHisThrGlyIleLeuLysIleValAlaGlnMetValAlaValTyr 140
Db 361 TCTTATAGAACTCAACACTGAGTGGGTCTTGAAGATTGTTACTCTGATGGCGCTTGG 420
Qy 141 IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTrpLysAsnSer 160
Db 421 GTGCTGGCTTCTTAGTGAATGGGCAATGATTTCTAGTTTTCAGATCTTTGGAAGGATGAA 480
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QY 161 ThrAsnThrGluGluCysGluProGlyPheValThrGluTrpTyrIleLeuAlaIleThr 180
Db 481 GGTAGT-----GAATGTGAACCTGGATTTTTTTCGGAATGGTACATCTCTTGCATCACA 534

QY 181 AlaPheLeuGluPheLeuLeuProValSerLeuValValTyrPheSerValGlnIleTyr 200
Db 535 TCATTCTTGGANNTGGATCCAGTCATCTTAGTCCTTATTTCAACATGAATATTTAT 594

QY 201 TrpSerLeuTrpLysArgGlySerLeuSerArgCysProSerHisAlaGlyPheIleAla 220
Db 595 TGGAGCCTGTGGAAGCGTGATCTCAGTAGGTGCCAAAGCCATCTCTGGACTGACTGCT 654

QY 221 ThrSerSerArgGlyThrGlyHisSerArgThrGlyLeuAlaCysArgThrSerLeu 240
Db 655 GTCTCTTCCAACATCTGTGACACTCATTCAGAGGTAGACTATCTTCAAGGAGATCTCTT 714

QY 241 ProGlyLeuLysGluProAlaAlaSerLeuHisSerGluSerProArgGlyLysSerSer 260
Db 715 TCTGCATCGACAGAAGTTCCTGCATCTCTTCATTCAGAGACAGAGGAGAGAGTAGT 774

QY 261 LeuLeuValSerLeuArgThrHisMetSerGlySerIleIleAlaPheLysValGlySer 280
Db 775 CTCAATGTTTTCTCAAGAACCAAGATGAATAGCAATACAAATTCCTTCCAAATGGGTCC 834

QY 281 PheCysArgSerGluSerProValLeuHisGluArgGluHisValGluLeuLeuArgGly 300
Db 835 TTCTCCCAATCAGATTCTGTAGCTCTTCCACAAAGGGAACATGTTGAACCTGCTTAGAGCC 894

QY 301 ArgLysLeuAlaArgSerLeuAlaValLeuLeuSerAlaPheAlaIleCysTrpAlaPro 320
Db 895 AGAGATAGCCAAAGTCACCTGGCCATCTCTTAGGGGTTTTTCTGTTCTGGCTGCCA 954

QY 321 TyrCysLeuPheThrIleValLeuSerThrTyrArgArgGlyGluArgProLysSerIle 340
Db 955 TATCTCTGTTCACAAATGTCCTTCAATTTATTCCTCAGCAACAGCTCTCAATCAGTT 1014

QY 341 TrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerLeuIleAsnProPheLeuTyr 360
Db 1015 TGGTATAGAAATTCATTTTGGCTTCAGTGGTTCAATTCCTTTGTCATCTCTTTGTAT 1074

QY 361 ProLeuCysHisArgArgPheGlnLysAlaPheTrpLysIleLeuCysValThrLysGln 380
Db 1075 CCATTGTGTCACAGCGCTTCAAGGCGTTCTTGAAAAATTTTGTATAAAAAAGCAA 1134

QY 381 ProAlaProSerGln---ThrGlnSerValSerSer 391
Db 1135 CCTCACCATCACACACACTCGGTCAATCTTCT 1170

RESULT 8
US-09-910-411-1
; Sequence 1, Application US/09910411
; Patent No. US20020137054A1
; GENERAL INFORMATION:
; APPLICANT: Bergsma, Derek
; APPLICANT: Fitzgerald, Laura
; APPLICANT: Li, Xiaotong
; APPLICANT: Michalovich, David
; APPLICANT: Zhu, Yuan
; TITLE OF INVENTION: AXOR35, A G-Protein Coupled Receptor
; FILE REFERENCE: GP70655-2C1
; CURRENT APPLICATION NUMBER: US/09/910,411
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: 09/693,761
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 09/497,790
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/431,898
; PRIOR FILING DATE: 1999-11-02
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1173
; TYPE: DNA
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; ORGANISM: Homo sapien
US-09-910-411-1
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## Alignment Scores:

Prod. No.:	4-25e-145	Length:	1173
Score:	1403.50	Matches:	271
Percent Similarity:	79.34%	Conservative:	40
Best Local Similarity:	69.13%	Mismatches:	78
Query Match:	68.63%	Indels:	3
DB:	9	Gaps:	2

US-10-626-126-9 (1-391) x US-09-910-411-1 (1-1173)

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QY 1 MetSerGluSerAsnGlyThrAspValLeuProLeuThrAlaGlnValProLeuAlaPhe 20
Db 1 ATGCCAGATACATAATAGCAACAATCAATTTATCACTAAGCACTCGTGTACTTTAGCATTT 60

QY 21 LeuMetSerLeuLeuAlaPheAlaIleThrIleGlyAsnAlaValValIleLeuAlaPhe 40
Db 61 TTTATGTCTTGTAGTCTTTTGTCTATAATGCTAGGAAATGCTTTGGTCATTTTAGCTTTT 120

QY 41 ValAlaAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60
Db 121 GTGGTCGACAAAACCTTAGACATCGAGTAGTATATTTTCTTAACCTGGCCATCTCT 180

QY 61 AspPhePheValGlyValIleSerIleProLeuTyrIleProHisThrLeuPheAsnTrp 80
Db 181 GACTTCTTTGGTGTGATCTCCATTCTTGTATCATCCTCACACGCTGTTTCAATGG 240

QY 81 AsnProGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrIleLeuCysThrAla 100
Db 241 GATTTGGGAAGGAATCTGTGATTTTGGCTCACACTGACTATCTGTTATGTACAGCA 300

QY 101 SerValTyrSerIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120
Db 301 TCTGTATATAACATGTCCTCATCAGCATGATCGATCTGTCAGTCTCAATAGCTGTG 360

QY 121 ArgTyrArgAlaGlnHisThrGlyIleLeuLysIleValAlaGlnMetValAlaValTrp 140
Db 361 TCTTATAGAACTCAACATACTGGGTCTTGAAGATTGTTACTCTGATGGTGGCGTTGG 420

QY 141 IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTrpLysAsnSer 160
Db 421 GTCTGGCTCTTCTAGTGAATGGCCAATGATTTCTTAGTTTCAGAGTCTTGGAAAGGAA 480

QY 161 ThrAsnThrGluGluCysGluProGlyPheValThrGluTrpTyrIleLeuAlaIleThr 180
Db 481 GGTAGT-----GAATGTGAACCTGGATTTTTTTCGGAATGGTACATCTTGCATCACA 534

QY 181 AlaPheLeuGluPheLeuLeuProValSerLeuValValTyrPheSerValGlnIleTyr 200
Db 535 TCATTCTTGGANNTGGATCCAGTCATCTTAGTCCTTATTTCAACATGAATATTTAT 594

QY 201 TrpSerLeuTrpLysArgGlySerLeuSerArgCysProSerHisAlaGlyPheIleAla 220
Db 595 TGGAGCCTGTGGAAGCGTGATCTCAGTAGGTGCCAAAGCCATCTCTGGACTGACTGCT 654

QY 221 ThrSerSerArgGlyThrGlyHisSerArgThrGlyLeuAlaCysArgThrSerLeu 240
Db 655 GTCTCTTCCAACATCTGTGACACTCATTCAGAGGTAGACTATCTTCAAGGAGATCTCTT 714

QY 241 ProGlyLeuLysGluProAlaAlaSerLeuHisSerGluSerProArgGlyLysSerSer 260
Db 715 TCTGCATCGACAGAAGTTCCTGCATCTCTTCAATTCAGAGACAGAGGAGAGAGTAGT 774

QY 261 LeuLeuValSerLeuArgThrHisMetSerGlySerIleIleAlaPheLysValGlySer 280
Db 775 CTCAATGTTTTCTCAAGAACCAAGATGAATAGCAATACAAATTCCTTCCAAATGGGTCC 834

QY 281 PheCysArgSerGluSerProValLeuHisGluArgGluHisValGluLeuLeuArgGly 300
Db 835 TTCTCCCAATCAGATTCTGTAGCTCTTCCACAAAGGGAACATGTTGAATCTGCTTAGAGCC 894
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QY 301 ArgLysLeuAlaArgSerLeuAlaValLeuLeuSerAlaPheAlaIleCysTrpAlaPro 320  
DB 895 AGAGATTAGCAAGTCACTGCCATCTCTAGGGTTTTCCTGGTGGCTCA 954  
QY 321 TyrCysLeuPheThrIleValLeuSerThrTyrArgArgGlyGluArgProLysSerIle 340  
DB 955 TATTCTCTGTTCAAAATGCTCTTTCATTTTATCTCTCAACAGGCTCTAAATCAGTT 1014  
QY 341 TrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerLeuIleAsnProPheLeuTyr 360  
DB 1015 TGGTAGAATGCAATTTGGCTTCAGTGGTTCAATTCCTTTGTCAATCTCTTTGTAT 1074  
QY 361 ProLeuCysHisArgPheGlnLysAlaPheTrpLysIleLeuCysValThrLysGln 380  
DB 1075 CCATTGTGTACAGCGCTTTCAAAGGCTTCTTGAATAATTTTGTATATAAAGCAA 1134  
QY 381 ProAlaProSerGln---ThrGlnSerValSerSer 391  
DB 1135 CCTCTACCATCACACACAGTCGGTCAGTATCTTCT 1170

## RESULT 9

US-09-875-076-13  
; Sequence 13, Application US/09875076  
; Publication No. US20030017528A1  
; GENERAL INFORMATION:  
; APPLICANT: Chen, Ruoping  
; APPLICANT: Dang, Huong T.  
; APPLICANT: Liaw, Chen W.  
; APPLICANT: Lin, I-Lin  
; TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors  
; FILE REFERENCE: AREN0050  
; CURRENT APPLICATION NUMBER: US/09/875,076  
; CURRENT FILING DATE: 2001-06-06  
; PRIOR APPLICATION NUMBER: 09/417,044  
; PRIOR FILING DATE: 1999-10-12  
; PRIOR APPLICATION NUMBER: 60/120,416  
; PRIOR FILING DATE: 1999-02-16  
; PRIOR APPLICATION NUMBER: 60/121,851  
; PRIOR FILING DATE: 1999-02-26  
; PRIOR APPLICATION NUMBER: 60/123,946  
; PRIOR FILING DATE: 1999-03-12  
; PRIOR APPLICATION NUMBER: 60/123,949  
; PRIOR FILING DATE: 1999-03-12  
; PRIOR APPLICATION NUMBER: 60/136,436  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/136,437  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/136,439  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/136,567  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/137,127  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/137,131  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/141,448  
; PRIOR FILING DATE: 1999-06-29  
; PRIOR APPLICATION NUMBER: 60/156,653  
; PRIOR FILING DATE: 1999-09-29  
; PRIOR APPLICATION NUMBER: 60/156,633  
; PRIOR FILING DATE: 1999-09-29  
; PRIOR APPLICATION NUMBER: 60/156,555  
; PRIOR FILING DATE: 1999-09-29  
; PRIOR APPLICATION NUMBER: 60/156,634  
; PRIOR FILING DATE: 1999-09-29  
; PRIOR APPLICATION NUMBER: 60/157,280  
; PRIOR FILING DATE: 1999-10-01  
; PRIOR APPLICATION NUMBER: 60/157,294  
; PRIOR FILING DATE: 1999-10-01  
; PRIOR APPLICATION NUMBER: 60/157,281  
; PRIOR FILING DATE: 1999-10-01  
; PRIOR APPLICATION NUMBER: 60/157,293  
; PRIOR FILING DATE: 1999-10-01

; PRIOR APPLICATION NUMBER: 60/157,282  
; PRIOR FILING DATE: 1999-10-01  
; NUMBER OF SEQ ID NOS: 74  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 13  
; LENGTH: 1173  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; US-09-875-076-13  
Alignment Scores:  
Pred. No.: 4,25e-145 Length: 1173  
Score: 1403.50 Matches: 271  
Percent Similarity: 79.34% Conservative: 40  
Best Local Similarity: 69.13% Mismatches: 78  
Query Match: 68.63% Indels: 3  
DB: 10 Gaps: 2  
US-10-626-126-9 (1-391) x US-09-875-076-13 (1-1173)  
QY 1 MetSerGluSerAsnGlyThrAspValLeuProLeuThrAlaGlnValProLeuAlaPhe 20  
DB 1 ATGCCAGATACCTAATAGCACCAATCAATTTATCACTAAGCACCTCGTGTACTTTAGCATTT 60  
QY 21 LeuMetSerLeuLeuAlaPheAlaIleThrIleGlyAsnAlaValIleLeuAlaPhe 40  
DB 61 TTTATGTCTTAGTAGCTTTTGTATATATGCTAGGAAATGCTTTGTCTCATTTTAGCTTTT 120  
QY 41 ValAlaAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60  
DB 121 GTGGTGGACAAAACCTTAGACATCGAAGTAGTATTTTCTTAACCTTGCCATCTCT 180  
QY 61 AspPhePheValGlyValIleSerIleProLeuTyrIleProHisThrLeuPheAsnTrp 80  
DB 181 GACTTCTTTGTGGGTGTGATCTCCATTCCTTTGTATACCTCCCTCACACGCTGTTCGAATGG 240  
QY 81 AsnProGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeuLeuCysThrAla 100  
DB 241 GATTTTGGAAAGGAAATCTGTGTATTTTGGCTCACTACTGACTATCTGTATGTACAGCA 300  
QY 101 SerValTyrSerIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120  
DB 301 TCTGTATATAACATGTTCTCTCATCAGTATGATGATGATGATGATGATGATGATGATGATG 360  
QY 121 ArgTyrArgAlaGlnHisThrGlyIleLeuLysIleValAlaGlnMetValAlaValTrp 140  
DB 361 TCTTATAGAACTCAACATATCGGGTCTTGAAGATTGTTACTCTGATGTCGCCGTTTGG 420  
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DB 421 GTGCTGGCTTCTTAGTGAATGGGCCAATGATTTCTAGTTTCAGAGTCTTGGAAAGATGAA 480  
QY 161 ThrAsnThrGluGluCysGluProGlyPheValThrGluTrpTyrIleLeuAlaIleThr 180  
DB 481 GGTAGT-----GAATGTGAACCTCGATTTTTTTCGGAATGTTGATCATCTTCCCATCACA 534  
QY 181 AlaPheLeuGluPheLeuLeuProValSerLeuValValTyrPheSerValGlnIleTyr 200  
DB 535 TCATTTCTTGAATTCGTGATCCAGTCATCTTTAGTCGCTATTTTCAACATGAATATTTAT 594  
QY 201 TrpSerLeuTrpLysArgGlySerLeuSerArgCysProSerHisAlaGlyPheIleAla 220  
DB 595 TGGAGCCTGTGGAAAGCGGTGATCATCTCAGTAGTGTCCAAAGCCATCCTCGACTGCTGT 654  
QY 221 ThrSerSerArgGlyThrGlyHisSerArgArgThrGlyLeuAlaCysArgThrSerLeu 240  
DB 655 GTCTCTTCCAAACATCTGTGGACACCTCATTCAGAGGTAGACTATCTTCAAGGAGATCTCTT 714  
QY 241 ProGlyLeuLysGluProAlaAlaSerLeuHisSerGluSerProArgGlyLysSerSer 260  
DB 715 TCTGCATCGACAGAAAGTTCTCTGCTCTTTCATTCAGAGAGACAGAGAGAAAGATAGT 774  
QY 261 LeuLeuValSerLeuArgThrHisMetSerGlySerIleIleAlaPheLysValGlySer 280

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Db 775 CTATGTTTCTCAGAACCAAGATGAATAGCAATACAAATGCTTCCAAAATGGGTTC 834
Qy 281 PheCysArgSerGluSerProValLeuHisGlnArgGluHisValGluLeuLeuArgGly 300
Db 835 TTCTCCCAATCAGATCTGTAGCTTTCACCAAGGGAACATGTTGAACCTGCTTAGAGCC 894
Qy 301 ArgGlyLeuAlaArgSerLeuAlaValLeuLeuSerAlaPheAlaIleCysTrpAlaPro 320
Db 895 AGGAGATAGCAAGTCACTGGCCATTCTCTTAGGGGTTTTGCTGTGTTCTGGGTCCA 954
Qy 321 TyrCysLeuPheThrIleValLeuSerThrTyrArgArgGlyGluArgProLysSerIle 340
Db 955 TATCTCTGTTCACAAATGCTTCATTTTATCTCAGCAACAGCTCCTAAATCAGIT 1014
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Db 1015 TGGTATAGTAATTCATTTTGGCTTCAGTGGTTCATTTCTCAATCTCTTTTGTAT 1074
Qy 361 ProLeuCysHisArgArgPheGlnLysAlaPheTrpLysIleLeuCysValThrLysGln 380
Db 1075 CCATTGTGTCAACAGCGCTTCAAAAGGCTTCTTGAATAATTTTGTATAAAAAAGCAA 1134
Qy 381 ProAlaProSerGln---ThrGlnSerValSerSer 391
Db 1135 CCTCTACCATCACACACAGCTGGTCAGTATCTTCT 1170

RESULT 10
US-09-876-252-13
; Sequence 13, Application US/09876252
; Publication No. US20030018182A1
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Lehmann-Bruinsma, Karin
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Lowitz, Kevin P.
; APPLICANT: Lin, I-Lin
; APPLICANT: Dang, Huong T.
; APPLICANT: Chen, Ruoping
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: Non-Endogenous Constitutively Activated Human G Protein Coupled Re
; FILE REFERENCE: AREN-0054
; CURRENT APPLICATION NUMBER: US/09/876,252
; CURRENT FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 09/416,760
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: 60/110,060
; PRIOR FILING DATE: 1998-11-27
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,852
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/109,213
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: 60/123,944
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,945
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,948
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,951
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,946
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,949
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/152,524
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: 60/151,114
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: 60/108,029
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; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: 60/136,436
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,439
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,567
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/137,127
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/137,131
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/141,448
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: 60/136,437
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/156,555
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,634
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,653
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/157,280
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,294
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,281
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,282
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/156,633
; PRIOR FILING DATE: 1999-09-29
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 13
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-876-252-13
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## Alignment Scores:

Pred. No.:	4,25e-145	Length:	1173
Score:	1403.50	Matches:	271
Percent Similarity:	79.34%	Conservative:	40
Best Local Similarity:	69.13%	Mismatches:	78
Query Match:	68.63%	Indels:	3
DB:	10	Gaps:	2

US-10-626-126-9 (1-391) x US-09-876-252-13 (1-1173)

Qy	1	MetSerGluSerAsnGlyThrAspValLeuProLeuThrAlaGlnValProLeuAlaPhe	20
Db	1	ATGCCAGATACATAAGCAATCAATTTATCACTAAGCACTCGTGTACTTTAGCATTT	60
Qy	21	LeuMetSerLeuLeuAlaPheAlaIleThrIleGlyAsnAlaValValIleLeuAlaPhe	40
Db	61	TTTATGTCTTAGTAGCTTTTGTCTAATAATGCTAGGAAATGCTTTGGTCATTTTGGCTTTT	120
Qy	41	ValAlaAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer	60
Db	121	GTGGTGGACAAACCTTAGACATCGAAGTAGTATTTTTTTTCTTAACCTTGGCACTCT	180
Qy	61	AspPhePheValGlyValIleSerIleProLeuTyrIleProHisThrLeuPheAsnTrp	80
Db	181	GACTTCTTTGTGGGTGTGATCTCCATTCCTTTGTACATCCCTCACAGCTGTTTCAATGG	240
Qy	81	AsnProGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeuLeuCysThrAla	100
Db	241	GATTTGGAAAGGAAATCTGTGATTTTGGCTCACTACTGACTATCTGTGTATGTACAGCA	300
Qy	101	SerValTyrSerIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal	120
Db	301	TCGTATATAACATTTGCTCTCATCTGATCGATACCTGCTGCTCAATGCTGCTGCTG	360

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QY 121 ArgTyrArgAlaGlnHisThrGlyIleLeuLysIleValAlaGlnMetValAlaValTyr 140
DB 361 TCTTATAGAACTCAACATACCTGGGCTCTGAAGATTGTACTCTGATGGTGCCGTTGG 420

QY 141 IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTrpLysAsnSer 160
DB 421 GTGCTGGCCTCTTAGTGAATGGGCCAATGATCTTAGTTTCAGAGTCTTTGGGAAGGATGAA 480

QY 161 ThrAsnThrGluGluCysGluProGlyPheValThrGluTrpTyrIleLeuAlaIleThr 180
DB 481 GGTAGT-----GAATGTGAACCTGGATTTTTCGGAATGGTACATCCTGCCATCACA 534

QY 181 AlaPheLeuGluPheLeuProValSerLeuValValTyrPheSerValGlnIleTyr 200
DB 535 TCATTCTTGGAAATTTGGATCCAGATCATCTTAGTCGCTATTATTTCAACATGAATATTAT 594

QY 201 TrpSerLeuTrpLysArgGlySerLeuSerArgCysProSerHisAlaGlyPheIleAla 220
DB 595 TGGAGCCTGTGAAGCGTGATCATCTCAGTAGGTGCCAAAGCCATCCTGGAGTACTGCT 654

QY 221 ThrSerArgGlyThrGlyHisSerArgArgThrGlyLeuAlaCysArgThrSerLeu 240
DB 655 GTCTTCTTCAACATCTGTGGACACTCATTCAGAGGTAGACTATCTTCAAGGAGATCTCTT 714

QY 241 ProGlyLeuLysGluProAlaAlaSerLeuHisSerGluSerProArgGlyLysSerSer 260
DB 715 TCTGCATCGACAGAGTCTCTGCATCCTTTCATTTCAGAGAGCAGAGGAGAAGAGTAGT 774

QY 261 LeuLeuValSerLeuArgThrHisMetSerGlySerIleIleAlaPheLysValGlySer 280
DB 775 CTCATGTTTCTCAAGAACCAAGATGAATAGCAATACAAATTCCTTCCAAAATGGGTTC 834

QY 281 PheCysArgSerGluSerProValLeuHisGlnArgGluHisValGluLeuLeuArgGly 300
DB 835 TTCCTCCATCAGATCTGTAGCTCTTCCACCAAGGGAAACATGTTGAACCTGCTTAGAGCC 894

QY 301 ArgLysLeuAlaArgSerLeuAlaValLeuLeuSerAlaPheAlaIleCysTrpAlaPro 320
DB 895 AGAGATTAGCAAGTCACTAGCCATCTCTTAGGGGTTTTCGTGTTTGTCTGGGCTCCA 954

QY 321 TyrCysLeuPheThrIleValLeuSerThrTyrArgArgGlyGluArgProLysSerIle 340
DB 955 TATCTCTCTTCACAATTCCTCTTTCATTTTATCTCTCAGCAACAGGTCTCTAAATCAGTT 1014

QY 341 TrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerLeuIleAsnProPheLeuTyr 360
DB 1015 TGGTATAGAAATGGCAATTTTGGCTTCAGTGGTTCATTTCTTTGTCAATCTCTTTTGTAT 1074

QY 361 ProLeuCysHisArgArgPheGlnLysAlaPheTrpLysIleLeuCysValThrLysGln 380
DB 1075 CCATTGTGTACAGGCGCTTCCAAAGGCTTTCTTGAATAATTTTGTATATAAAGCAA 1134

QY 381 ProAlaProSerGln---ThrGlnSerValSerSer 391
DB 1135 CCTCATCATCACACACAGTCGGTCAGTATCTTCT 1170
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## RESULT 11

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US-10-052-193-1
; Sequence 1, Application US/10052193
; Publication No. US20020132755A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer, Inc.
; TITLE OF INVENTION: HISTAMINE RECEPTOR ANTAGONISTS
; FILE REFERENCE: PC10963A
; CURRENT APPLICATION NUMBER: US/10/052,193
; CURRENT FILING DATE: 2002-01-17
; PRIOR APPLICATION NUMBER: 0101223.6
; PRIOR FILING DATE: 2001-01-17
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1173
; TYPE: DNA
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; ORGANISM: Homo sapiens
US-10-052-193-1
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## Alignment Scores:

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Pred. No.: 4,25e-145 Length: 1173
Score: 1403.50 Matches: 271
Percent Similarity: 79.34% Conservative: 40
Best Local Similarity: 69.13% Mismatches: 78
Query Match: 68.63% Indels: 3
DB: 13 Gaps: 2
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US-10-626-126-9 (1-391) x US-10-052-193-1 (1-1173)

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QY 1 MetSerGluSerAsnGlyThrAspValLeuProLeuThrAlaGlnValProLeuAlaPhe 20
DB 1 ATGCCAGATCAATAATAGCACAAATCAATTTATCACTAAGCACTCGTGTACTTTAGCATTT 60

QY 21 LeuMetSerLeuLeuAlaPheAlaIleThrIleGlyAsnAlaValIleLeuAlaPhe 40
DB 61 TTTATGTCCTTAGTAGCTTTTGTATATAATGCTAGGAATGCTTTGGTCATTTTAGCTTTT 120

QY 41 ValAlaAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60
DB 121 GTGGTGGACAAAACCTTAGACATCGAAGTAGTTATTTTCTTAACCTTGCCATCTCT 180

QY 61 AspPhePheValGlyValIleSerIleProLeuTyrIleProHisThrLeuPheAsnTrp 80
DB 181 GACTTCTTTGTGGGTGATCTCCATTCCTTTGTATACATCCCTCCACGCTGTTCGAATGG 240

QY 81 AsnProGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeuLeuCysThrAla 100
DB 241 GATTTTGGAAAGGAATCTGTGATTTTGGTCACTACTGACTATCTGTTATGTACAGCA 300

QY 101 SerValTyrSerIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120
DB 301 TCTGTATATAACATGTCTCATCAGTATGATGATACCTGCTCAGTCTCAAAATGCTGTG 360

QY 121 ArgTyrArgAlaGlnHisThrGlyIleLeuLysIleValAlaGlnMetValAlaValTyr 140
DB 361 TCTTATAGAACTCAACATACCTGGGCTCTTGAAGATTGTTCCTCTGATGGTGCCGTTGG 420

QY 141 IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTrpLysAsnSer 160
DB 421 GTGCTGGCCTCTTAGTGAATGGGCCAATGATCTTAGTTTCAGAGTCTTTGGGAAGGATGAA 480

QY 161 ThrAsnThrGluGluCysGluProGlyPheValThrGluTrpTyrIleLeuAlaIleThr 180
DB 481 GGTAGT-----GAATGTGAACCTGGATTTTTCGGAATGGTACATCCTTGCCATCACA 534

QY 181 AlaPheLeuGluPheLeuProValSerLeuValValTyrPheSerValGlnIleTyr 200
DB 535 TCATTCTTGGAAATTCGTATCCAGTCACTCTTAGTCGCTTATTTCAACATGAATATTAT 594

QY 201 TrpSerLeuTrpLysArgGlySerLeuSerArgCysProSerHisAlaGlyPheIleAla 220
DB 595 TGGAGCCTGTGAAGCGTGATCATCTCAGTAGGTGCCAAAGCCATCCTGGAGTACTGCT 654

QY 221 ThrSerArgGlyThrGlyHisSerArgArgThrGlyLeuAlaCysArgThrSerLeu 240
DB 655 GTCTCTTCCAAACATCTGTGGACACTCATTCAGAGGTAGACTATCTTCAAGGAGATCTCTT 714

QY 241 ProGlyLeuLysGluProAlaAlaSerLeuHisSerGluSerProArgGlyLysSerSer 260
DB 715 TCTGCATCGACAGAGATTCCTGCATCCTTTCATTTCAGAGAGCAGAGGAGAAGAGTAGT 774

QY 261 LeuLeuValSerLeuArgThrHisMetSerGlySerIleIleAlaPheLysValGlySer 280
DB 775 CTCATGTTTCTCAAGAACCAAGATGAATACCAATACAAATTCCTTCCAAAATGGGTTC 834

QY 281 PheCysArgSerGluSerProValLeuHisGlnArgGluHisValGluLeuLeuArgGly 300
DB 835 TTCCTCCATCAGATCTGTAGCTCTTCCACCAAGGGAAACATGTTGAACCTGCTTAGAGCC 894
```

```
QY 301 ArgLysLeuAlaArgSerLeuAlaValLeuLeuSerAlaPheAlaIleCysTrpAlaPro 320
Db 895 AGAGATTAGCCAGTACCTGGCCATTCTCTTAGGGGTTTTTCTGCTGTTGCTGGCTCCA 954
QY 321 TyrCysLeuPheThrIleValLeuSerThrTyrArgArgGlyGluArgProLysSerIle 340
Db 955 TATTCTCTGTTCACAAATTGCTCTTTCATTTTATCTCAGCACACAGCTCTCAATCAGTT 1014
QY 341 TrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerLeuIleAsnPropheLeuTyr 360
Db 1015 TGGTATAGAAATTCGATTTTGGCTTCAGTGGTTCAAATTCCTTTGTCAATCCTCTTTGTAT 1074
QY 361 ProLeuCysHisArgArgPheGlnLysAlaPheTrpValIleLeuCysValThrLysGln 380
Db 1075 CCATTGTGCACAAAGCGCTTCAAAAGGCTTTCTTGAAAATATTTTGTATAAAAAGCAA 1134
QY 381 ProAlaProSerGln--ThrGlnSerValSerSer 391
Db 1135 CCTCTACCATCACAAACAGTCGCTCAGTATCTTCT 1170
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## RESULT 12

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US-10-272-983-13
; Sequence 13, Application US/10272983
; Publication No. US20030148450A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Dang, Huong T.
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
; FILE REFERENCE: AREN0050
; CURRENT APPLICATION NUMBER: US/10/272,983
; PRIOR FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: US/09/417,044
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 60/109,213
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,851
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/123,946
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,949
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/136,436
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,437
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,439
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,567
; PRIOR FILING DATE: 1999-05-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 13
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-272-983-13
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Alignment Scores:
Pred. No.: 4,25e-145 Length: 1173
Score: 1403.50 Matches: 271
Percent Similarity: 79.34% Conservative: 40
Best Local Similarity: 69.13% Mismatches: 78
Query Match: 68.63% Indels: 3
DB: 15 Gaps: 2
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US-10-626-126-9 (1-391) x US-10-272-983-13 (1-1173)

QY 1 MetSerGluSerAsnGlyThrAspValLeuProLeuThrAlaGlnValProLeuAlaPhe 20

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Db 1 ATGCCAGATTAATAAGCACAATCAATTTATCACTAAGCACTCGTGTACTTTAGCATTT 60
QY 21 LeuMetSerLeuLeuAlaPheAlaIleThrIleGlyAsnAlaValValIleLeuAlaPhe 40
Db 61 TTTATGTCTCTAGTAGCTTTTGTATATGCTAGGAAATGCTTTGCTCATTTAGCTTTT 120
QY 41 ValAlaAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60
Db 121 GTGGTGGACAAAACCTTAGACATCGAAGTAGTTATTTTCTTAACCTGGCCTCTCT 180
QY 61 AspPhePheValGlyValIleSerIleProLeuTyrIleProHisThrLeuPheAsnTrp 80
Db 181 GACTTCTTTGTGGGTGTGATCTCCATTCCTTTGTATACATCCCTCACACGCTGTTCGAATGG 240
QY 81 AsnProGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeuLeuCysThrAla 100
Db 241 GATTTTGGAAAGGAATCTGTGTATTTTGGCTCACTACTGACTATCTGTATGTACAGCA 300
QY 101 SerValTyrSerIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120
Db 301 TCTGTATATAACATTCCTCATCAGCTATGATCGATACCTGTCTCAGTCTCAAAATGCTGTG 360
QY 121 ArgTyrArgAlaGlnHisThrGlyIleLeuLysIleValAlaGlnMetValAlaValTrp 140
Db 361 TCTTATAGAACTCAACATACCTGGGTCTTGAAGATTGTACTCTGATGGTGGCGTTTGG 420
QY 141 IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTrpLysAsnSer 160
Db 421 GTGCTGGCCCTTCTTAGTGAATGGCCCAATGATCTAGTTTCAGAGTCTTGGAAAGGATGAA 480
QY 161 ThrAsnThrGluGluCysGluProGlyPheValThrGluTrpTyrIleLeuAlaIleThr 180
Db 481 GGTAGT-----GAATGTCAACTGGATTTTTCGGAATGGTACATCCTTGCATCACA 534
QY 181 AlaPheLeuGluPheLeuLeuProValSerLeuValValTyrPheSerValGlnIleTyr 200
Db 535 TCATTTCTTGGAAATTCGTATCCAGTCATCTTAGTCGCTTATTTCACATGAATATTAT 594
QY 201 TrpSerLeuTrpLysArgGlySerLeuSerArgCysProSerHisAlaGlyPheIleAla 220
Db 595 TGGAGCTGTGGAGCGTGATCATCTCAGTAGTGCAGAAAGCCATCCTGGACGTACTGCT 654
QY 221 ThrSerSerArgGlyThrGlyHisSerArgArgThrGlyLeuAlaCysArgThrSerLeu 240
Db 655 GTCTCTTCCACATCTGTGGACACTCATTCAGAGGTAGACTATCTTCAAGGAGATCTCTT 714
QY 241 ProGlyLeuLysGluProAlaAlaSerLeuHisSerGluSerProArgGlyLysSerSer 260
Db 715 TCTGCATCGACAGAAAGTTCTCTGCATCTTTCATTCAGAGAGACAGAGAGAGTAGT 774
QY 261 LeuLeuValSerLeuArgThrHisMetSerGlySerIleAlaPheLysValGlySer 280
Db 775 CTCATGTTTCTCAAGAACCAAGATGAATAGCAATACAAATGCTTCCAAATGGGTTC 834
QY 281 PheCysArgSerGluSerProValLeuHisGlnArgGluHisValGluLeuLeuArgGly 300
Db 835 TTCTCCCAATCAGATTCTGTAGCTCTTACCAAAAGGGAACATCTTGAACCTGCTTAGAGCC 894
QY 301 ArgLysLeuAlaArgSerLeuAlaValLeuLeuSerAlaPheAlaIleCysTrpAlaPro 320
Db 895 AGGAGATTAGCCAAAGTCACTGGCCATTCCTTAGGGGTTTTTCTGCTGCTGGCTCCA 954
QY 321 TyrCysLeuPheThrIleValLeuSerThrTyrArgArgGlyGluArgProLysSerIle 340
Db 955 TATTCTCTGTTTCACAATGTCTCTTTCATTTTATTCCTCAGCAACAGCTCTCAATCAGTT 1014
QY 341 TrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerLeuIleAsnPropheLeuTyr 360
Db 1015 TGGTATAGAAATTCGATTTTGGCTTCAGTGGTTCAAATTCCTTTGTCAATCCTCTTTGTAT 1074
QY 361 ProLeuCysHisArgArgPheGlnLysAlaPheTrpLysIleLeuCysValThrLysGln 380
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Db 1075 CCATTGTGTCAAGCGCTTTCAAAGGCTTTCTTGAATAATATTTTGTATATAAAGCAA 1134
Qy 381 ProAlaProSerGln---ThrGlnSerValSerSer 391
Db 1135 CCTCTACCATCAACAACAGCGTGGTCACTATCTTCT 1170

RESULT 13
US-10-354-769-1
; Sequence 1, Application US/10354769
; Publication No. US20030149242A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer Inc.
; APPLICANT: O'Reilly, Mark A.
; APPLICANT: Peter, Beate
; TITLE OF INVENTION: NOVEL POLYPEPTIDE
; FILE REFERENCE: PC10373B
; CURRENT APPLICATION NUMBER: US/10/354,769
; PRIOR FILING DATE: 2003-01-30
; PRIOR APPLICATION NUMBER: US 09/698,801
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/211,243
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: GB 9925641.4
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: GB 0009973.9
; PRIOR FILING DATE: 2000-04-20
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-354-769-1

Alignment Scores:
Pred. No.: 4,25e-145 Length: 1173
Score: 1403.50 Matches: 271
Percent Similarity: 79.34% Conservative: 40
Best Local Similarity: 69.13% Mismatches: 78
Query Match: 68.63% Indels: 3
DB: 15 Gaps: 2

US-10-626-126-9 (1-391) x US-10-354-769-1 (1-1173)
Qy 1 MetSerGluSerAsnGlyThrAspValLeuThrAlaGlnValProLeuAlaPhe 20
Db 1 ATGCCAGATCAATAAGACCAATCAATTTATCACTAAGCACTCGGTACTTACCTTTAGCATTT 60
Qy 21 LeuMetSerLeuLeuAlaPheAlaIleThrIleGlyAsnAlaValValIleLeuAlaPhe 40
Db 61 TTTATGTCTTAGTAGCTTTTCTATATAGCTAGGAAATGCTTTGGTCAATTTTAGCTTTT 120
Qy 41 ValAlaAspArgAsnLeuAlaArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60
Db 121 GTGGTGGACAAACCTTAGACATCAAGTAGTATATTTTCTTAACCTGGCCATCTCT 180
Qy 61 AspPhePheValGlyValIleSerIleProLeuTyrIleProHisThrLeuPheAsnTrp 80
Db 181 GACTTCTTTGGGTGTGATCTCCATTCCTTTGTATACATCCCTCACACGCTGTTTCAATGG 240
Qy 81 AsnProGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeuLeuCysThrAla 100
Db 241 GATTTTGGAAAGGAATCTGTGTATTTTGGCTCACTACTGACTATCTGTATGTATGACGA 300
Qy 101 SerValTyrSerIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120
Db 301 TCTGTATATACATTTGCTCATCAGCTATGATCATCTGCTGCTCAAGTCTCAAAATGCTGTG 360
Qy 121 ArgTyrArgAlaGlnHisThrGlyIleLeuValIleValAlaGlnMetValAlaValTrp 140
Db 361 TCTTATAGAACTCAACATCTAGGCTTGAAGATGTTTACTCTGATGGTGGCCGTGG 420
Qy 141 IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTrpLysAsnSer 160

US-10-393-807-13
; Sequence 13, Application US/10393807
; Publication No. US20030175891A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Dang, Huong T.
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
; FILE REFERENCE: AREN0050
; CURRENT APPLICATION NUMBER: US/10/393,807
; CURRENT FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: US/09/417,044
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 60/109,213
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,851
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/123,946

RESULT 14
US-10-393-807-13
; Sequence 13, Application US/10393807
; Publication No. US20030175891A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Dang, Huong T.
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
; FILE REFERENCE: AREN0050
; CURRENT APPLICATION NUMBER: US/10/393,807
; CURRENT FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: US/09/417,044
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 60/109,213
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,851
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/123,946

Db 421 GTGCTGGCGCTTCTTAGTCAATGGCCAAATGATTTCTAGTTTCAGAGTCTTTGGAAGGATCAA 480
Qy 161 ThrAsnThrGluGluCysGluProGlyPheValThrGluTyrTrpTyrIleLeuAlaIleThr 180
Db 481 GGTAGT-----GAATGTGAACCTGGATTTTTTTTGGAAATGGTATCATCTCTTGCCATCACA 534
Qy 181 AlaPheLeuGluPheLeuProValSerLeuValValTyrPheSerValGlnIleTyr 200
Db 535 TCATTTCTTGGAAATTCGTGATCCAGTCACTTAGTCGCTTATTTCAACATGAATATTTAT 594
Qy 201 TrpSerLeuTyrPlysArgGlySerLeuSerArgCysProSerHisAlaGlyPheIleAla 220
Db 595 TGGAGCCTGTGGAGCGTGATCATCTCAGTAGGTGCCAAAGCCATCTCTGGAGTACTGCT 654
Qy 221 ThrSerSerArgGlyThrGlyHisSerArgThrGlyLeuAlaCysArgThrSerLeu 240
Db 655 GTCTCTTCCAAACATCTGTGGACACTCATTTCAAGAGTAGACTATCTTCAAGGAGATCTCTT 714
Qy 241 ProGlyLeuLysGluProAlaSerLeuHisSerGluSerProArgGlyLysSerSer 260
Db 715 TCTGCATCGACAGAGTTCTCTGCATCTCTTCAAGAGACAGAGGAGAAAGATAGT 774
Qy 261 LeuLeuValSerLeuArgThrHisMetSerGlySerIleIleAlaPheLysValGlySer 280
Db 775 CTCATGTTTTCTCAAGAAACCAAGATGAATAGCAATACATTTGCTTCCAAATGGGTTCC 834
Qy 281 PheCysArgSerGluSerProValLeuHisGlnArgGluHisValGluLeuLeuArgGly 300
Db 835 TTCTCCCAATCAGATTTCTGTAGCTCTTCCACCAAGGGAACATGTTGAACTGCTTAGAGCC 894
Qy 301 ArgLysLeuAlaArgSerLeuAlaValLeuLeuSerAlaPheAlaIleCysTrpAlaPro 320
Db 895 AGGATTTAGCCAGTCACTGCTCATCTCTTAGGGGTTTTTCTGTTTCTGGGCTCCA 954
Qy 321 TyrCysLeuPheThrIleValLeuSerThrTyrArgArgGlyGluArgProLysSerIle 340
Db 955 TATTCTCTGTTTCAACAATTTGCTTTTCAATTTTATTTCTCAGCAACAGGTCCTAAATCAGTT 1014
Qy 341 TrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerLeuIleAsnProPheLeuTyr 360
Db 1015 TGGTATAGAATTCGATTTTGGCTTTCAGTGGTTCATTTCTTGTCAATCTCTTTTGTAT 1074
Qy 361 ProLeuCysHisArgArgPheGlnLysAlaPheTrpLysIleLeuCysValThrLysGln 380
Db 1075 CCATTTGTCTCAAGCGCTTTTCAAAAGGCTTTCTTGAATAATATTTTGTATATAAAGCAA 1134
Qy 381 ProAlaProSerGln---ThrGlnSerValSerSer 391
Db 1135 CCTCTACCATCAACAACAGCGTGGTCACTATCTTCT 1170
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```

221 ThrSerSerArgGlyThrGlyHisSerArgArgThrGlyLeuAlaCysArgThrSerLeu 240
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
655 GTCTCTTCCAACATCTGTGGACACTCATTCAGAGGTAGACTATCTTCAAGGAGATCTCT 714
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
241 ProGlyLeuLyGluProAlaAlaSerLeuHisSerGluSerProArgGlyLyvsSerSer 260
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
715 TCTGCATCGACAGAGTTCTCGATCTCTTTCATTTCAGAGAGACAGAGGAGAAAGATAGT 774
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
261 LeuLeuValSerLeuArgThrHisMetSerGlySerIleIleAlaPheLyvsValGlySer 280
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
775 CTATGTTTCTTCAAGAACCAAGATGAATAGCAATACAAATTGCTTCCAAAATGGGTTC 834
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
281 PheCysArgSerGluSerProValLeuHisGlnArgGluHisValGluLeuLeuArgGly 300
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
835 TTCTCCCAATCAGATTCTGTAGCTCTTCACCAAGGGAACATGTTGAACTGCTTAGAGCC 894
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
301 ArgLyLeuAlaArgSerLeuAlaValLeuLeuSerAlaPheAlaIleCysTrpAlaPro 320
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
895 AGAGATTAGCAAGATGCTGCCATTCTCTTAGGGGTTTTTGTCTGTCTGGGCTCCA 954
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
321 TyrCysLeuPheThrIleValLeuSerThrTyrArgArgGlyGluArgProLyvsSerIle 340
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
955 TATTCTCTGTTCACAATTGCTCTTTCATTATTCCTCAGCAACAGGTCCTAAATCAGTT 1014
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
341 TrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerLeuIleAsnPropheLeuTyr 360
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1015 TGTATAGAAATTGCATTTTGGCTTCAGTGGTTCAATTCCTTTGTGTCATCTCTTTTGTAT 1074
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361 ProLeuCysHisArgArgPheGlnLyAlaPheTrpLyIleLeuCysValThrLyvsGln 380
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1075 CCATTGTGTCAAGCGCTTTCAAAGGCTTTCTTGAAAATATTTTGTATAAAAAAGCAA 1134
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
381 ProAlaProSerGln---ThrGlnSerValSerSer 391
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1135 CCTCTACCATCACACACAGTGGTCAAGTATCTTCT 1170
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RESULT 15
US-10-417-820A-13
; Sequence 13, Application US/10417820A
; Publication No. US20030229216A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lowitz, Kevin
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Behan, Dominic P.
; TITLE OF INVENTION: Constitutively Activated Human G Protein Coupled
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: 7.US28.CON
; CURRENT APPLICATION NUMBER: US/10/417,820A
; CURRENT FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: 09/416,760
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: 60/110,060
; PRIOR FILING DATE: 1998-11-27
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,952
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/109,213
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: 60/123,944
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,945
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,948
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,951
; PRIOR FILING DATE: 1999-03-12
; Remaining Prior Application data removed - See File Wrapper or PALM.

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; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 13
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-417-820A-13

Alignment Scores:
Pred. No.:      4.25e-145      Length:      1173
Score:          1403.50      Matches:      271
Percent Similarity: 79.34%      Conservative:  70
Best Local Similarity: 69.13%      Mismatches:   48
Query Match:      68.63%      Indels:       3
DB:              17          Gaps:         2

US-10-626-126-9 (1-391) x US-10-417-820A-13 (1-1173)
Qy      1 MetSerGluSerAanGlyThrAspValLeuProLeuThrAlaGlnValProLeuAlaPhe 200
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      1 ATGCAGACTACTAATAGCACAACTCAATTTATCCTAAGCACTCGTGTTACTTTAGCATTT 60

Qy     21 LeuMetSerLeuLeuAlaPheAlaIleThrIleGlyAenAlaValValIleLeuAlaPhe 40
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db     61 TTTATGTCTTTAGTAGCTTTTGGCTATATAATGCTAGGAAATGCTTTGGTCATTTAGCTTTT 120

Qy     41 ValAlaAspArgAenLeuArgHisArgSerAenTyrPhePheLeuAenLeuAlaIleSer 60
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db    121 GTGGTGACAAACCTTAGACATCGAAGTAGTATTATTTTTTCTTAACTTGGCCATCTCT 180

Qy     61 AspPhePheValGlyValIleSerIleProLeuTyrIleProHisThrIleuPheAenTrp 80
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db    181 GACTTCTTTGTGGGTGTGATCTCCATCTCTTTGTATACATCCCTCACACGCTGTCGAATGG 240

Qy     81 AenProGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrIleuLeuCysThrAla 100
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db    241 GATTTTGGAAAGGAAATCTGTGATTTTGGGTCACTACTGACTATCTGTTATGTACAGCA 300

Qy    101 SerValTyrSerIleValLeuIleSerTyrAspArgTyrGlnSerValSerAenAlaVal 120
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db    301 TCTGTATATACTTGTCTCATACGATGATGATGATACCTGCTGAGTCTCAAAATGCTGTGG 360

Qy    121 ArgTyrArgAlaGlnHisThrGlyIleLeuIleValAlaGlnMetValAlaValTrp 140
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db    361 TCTTTATAGAACTCAACATACTGGGGTCTTTGAAGATTGTTACTCTGATGGTGCCGTGGT 420

Qy    141 IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTrpIysAenSer 160
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db    421 GTGCTGGCTTCTTAGTGAATGGGCCAAATGATTCCTAGTTCAGAGTCTTTGGGAAGGATGAA 480

Qy    161 ThrAenThrGluGluCysGluProGlyPheValThrGluTrpTyrIleLeuAlaIleThr 180
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db    481 GGTAGT-----GAATGTGAACCTGGATTTTTTTCGGAATGGTAGATCTCTGCCATCA 534

Qy    181 AlaPheLeuGluPheLeuLeuProValSerLeuValValTyrPheSerValGlnIleTyr 200
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db    535 TCATCTCTTGGAAATTCGTGATCCCACTCATCTTAGTCGCTTATTTCAACATGAATATTAT 594

Qy    201 TrpSerLeuTrpLysArgGlySerLeuSerArgCysProSerHisAlaGlyPheIleAla 220
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db    595 TGGAGCCTGTGGAGCGTGATCATCTCAGTAGGTGCCAAAGCCATCCTCGACTGCTGCT 654

Qy    221 ThrSerSerArgGlyThrGlyHisSerArgArgThrGlyLeuAlaCysArgThrSerLeu 240
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db    655 GTCTCTTCCAAACATCTGTGGACACTCATTCAGAGGTAGATCATCTTCAAGGAGATCTCT 714

Qy    241 ProGlyLeuLysGluProAlaAlaSerLeuHisSerGluSerProArgGlyLysSerSer 260
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db    715 TCTGCATCGACAGAAGTTCTCGCATCTTTCATTCCAGAGACAGACAGGAGAGAGTAGT 774

Qy    261 LeuLeuValSerLeuArgThrHisMetSerGlySerIleIleAlaPheLysValGlySer 280
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db    775 CTCATGTTTCTCCTCAAGAACCAAGATGAATGATCAATCAATTTGCTTCCAAATGGGTGTC 834

```

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 3, 2005, 01:38:32 ; Search time 41 Seconds  
(without alignments)  
917.579 Million cell updates/sec

Title: US-10-626-126-9  
Perfect score: 2045  
Sequence: 1 MSESNGTDVLP LTAQVPLAF.....WKILCVTKQAPSPQTSVSS 391

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1403.5	68.6	390	JC7566	histamine H4 recep
2	410.5	20.1	590	S47572	muscarinic acetyl
3	408.5	20.0	590	S01114	muscarinic acetyl
4	407.5	19.9	589	A29476	muscarinic acetyl
5	403.5	19.7	590	S10128	muscarinic acetyl
6	401.5	19.6	491	A41632	histamine H1 recep
7	401	19.6	531	JT0531	muscarinic acetyl
8	397.5	19.4	589	B29514	muscarinic acetyl
9	395.5	19.3	487	JC2495	histamine H1 recep
10	395	19.3	532	JT0530	muscarinic acetyl
11	390.5	19.1	386	A42688	serotonin receptor
12	389.5	19.0	460	A24325	muscarinic acetyl
13	389	19.0	639	A55019	muscarinic acetyl
14	388.5	19.0	460	S09508	muscarinic acetyl
15	388	19.0	501	T18863	hypothetical prote
16	387.5	18.9	386	T18637	serotonin receptor
17	387.5	18.9	390	JN0268	serotonin receptor
18	385.5	18.9	460	I51937	muscarinic recepto
19	385.5	18.9	460	A29514	muscarinic acetyl
20	383	18.7	486	JC1415	histamine H1 recep
21	382.5	18.7	488	I56507	histamine H1 recep
22	380.5	18.6	386	S54153	serotonin receptor
23	377	18.4	501	JH0447	alpha-1A-adrenergi
24	377	18.4	572	T139369	alpha-1A-adrenergi
25	375.5	18.4	477	S71323	serotonin receptor
26	374.5	18.3	389	S68422	alpha-1A adrenergi
27	374.5	18.3	560	A38731	alpha-1A adrenergi
28	373.5	18.3	460	A31897	muscarinic acetyl
29	372.5	18.2	515	A40491	alpha-1-adrenergi

30	369.5	18.1	390	2	S58126	serotonin receptor
31	368.5	18.0	517	2	A45121	alpha-1B adrenergi
32	363.5	17.8	366	2	A47385	serotonin receptor
33	362.5	17.7	515	2	JC1525	alpha-1B-adrenergi
34	361.5	17.7	379	2	JC6178	serotonin receptor
35	361	17.7	466	2	S10126	muscarinic acetyl
36	359	17.6	377	2	A53279	serotonin receptor
37	358.5	17.5	366	2	S26048	serotonin receptor
38	358.5	17.5	479	2	S33776	muscarinic acetyl
39	357.5	17.5	366	2	A47321	serotonin receptor
40	357.5	17.5	429	2	S65656	alpha-1C-adrenergi
41	357.5	17.5	466	2	JN0765	alpha-1C-adrenergi
42	357.5	17.5	466	2	S10856	muscarinic acetyl
43	357.5	17.5	499	2	S65657	alpha-1C-adrenergi
44	356.5	17.4	466	2	A40972	muscarinic acetyl
45	356	17.4	377	2	B30341	G protein-coupled

ALIGNMENTS

RESULT 1

JC7566  
histamine H4 receptor, HH4R - human  
C:Species: Homo sapiens (man)  
C>Date: 30-Jun-2001 #sequence\_revision 30-Jun-2001 #text\_change 09-Jul-2004  
C:Accession: JC7566  
R:Nakamura, T.; Itadani, H.; Hidaka, Y.; Ohta, M.; Tanaka, K.  
Biochem. Biophys. Res. Commun. 279, 615-620, 2000  
A:Title: Molecular cloning and characterization of a new human histamine receptor, HH4R.  
A:Reference number: JC7566; MUID: 20568725; PMID:1118334  
A:Contents: Leukocyte  
A:Accession: JC7566  
A:Molecule type: mRNA  
A:Residues: 1-390 <NAK>  
A:Cross-references: UNIPROT:Q9H3N8; DDBJ:AB045370  
C:Comment: This receptor, belonging to the biogenic amine receptors of G protein-coupled  
C:Genetic: hh4r  
A:Gene: hh4r  
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match	68.6%	Score	1403.5	DB	2	Length	390
Best Local Similarity	69.1%	Pred. No.	7.4e-112				
Matches	271	Conservative	40	Mismatches	78	Indels	3
Gaps	2						
Qy	1	MSESNGTDVLP LTAQVPLAF LMSLLAFATIGNAVVILAFVADRNLRHRSNYFFLNLAIS	60				
Db	1	MPDTNSTINLSLSTRVTLLAFFMSLVAFALMGNALVILAFVVDKRLHRSSYFFLNLAIS	60				
Qy	61	DFPVGVISIPLYIPHTLFNNPGSGICMFWLITDYLLCTASVYSIVLISYDRYOSVSNV	120				
Db	61	DFPVGVISIPLYIPHTLFNWDGKICVFWLTDTLLCTASVYVNIIVLISYDRYLSVSNV	120				
Qy	121	RYPAQHTGILKVAQVAVVILAFVNGPMILASDSWKSNSTNTECEPGVPTWYILAIT	180				
Db	121	SYRTQHTGVLKIVTLVAVVAVLAFVNGPMILVSESKDEGS--ECEPGFSEWYILAIT	178				
Qy	181	AFLEFLLPSLVVYFVSQIYWSLWKRGSLRCPSHAGFIATSSRGTCGHSRRTGLACRTSL	240				
Db	179	SFLFVPIVLVAFVFNWYWSLWKDKDHLRCSQSHFGLTAVSSNICGHSFGRLSRSL	238				
Qy	241	PGLEKPAALHSSPRGKSLVLSLRTHMSGSIAPKVGSCFRCSESPVLHOREHVELLRG	300				
Db	239	SASTVEPASFHSRQRKSLMFSRRTKWSNNTIASKMGFSQSQSDSVLHOREHVELLRA	298				
Qy	301	RKLARSIALVLSAFACWAPYCLFTIVLSTYRGERPKSIWYSIAFWLQWNSLIINPFY	360				
Db	299	RLAKSLAILLGVFAVCWAPYSLFTIVLSFYSSATGPKSVWYRIAPFWLQWNSFVNPLLY	358				
Qy	361	PLCHRRFQKAFWKILCVTKQAPSPQ-TQSVSS 391					
Db	359	PLCHKRFQAKFLKIFCIKKQPLSPQHSRVS 390					



```
F;195-207/Domain: transmembrane #status predicted <TM>
F;231-252/Domain: transmembrane #status predicted <TM>
F;493-513/Domain: transmembrane #status predicted <TM>
F;525-546/Domain: transmembrane #status predicted <TM>
F;5,6,15,41/Binding site: carbohydrate (Asn) #status predicted

Query Match      19.7%; Score 403.5; DB 2; Length 590;
Best Local Similarity 24.3%; Pred. No. 1.6e-26;
Matches 131; Conservative 85; Mismatches 163; Indels 161; Gaps 19;

QY   2 SESNGTDLPLTAQ-----VPLAFLMSLLAFATTIGNAVVILAFVADRNLRHRSNYFFLN 56
Db    |||:|||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY   50 SSPDGTDDPLGHTVMQVVFIAPLIGILALVTIIGNILVFSEKVKRQKTVMNYPFLS 109
Db    |||:|||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY   57 LAISDFPVGVGISIPLYPHTLFN-WNPGSICMFWLITDYLLCTASYSIVLSIDRYQS 115
Db    |||:|||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY   110 LACADLIIGVISMNLFTYIIIMRWALGNLCADLWLAIDVVASNASVMNLLVISFDVFS 169
Db    |||:|||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY   116 VSNVRYRAQHTGIKLVAQKVAV-NILAFLVNGPMILLASDW-----KNSTWERCEPG 169
Db    :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY   170 ITRPLTYRAKRT--TKRAGVMIGLAWVISFVLWAPAIL---FMQYFVGKRTVPPEGCFIQ 224
Db    |||:|||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY   170 FVTEWYLAIATFLEFLLPVSLVVYFSVOIYWSLWKR----- 206
Db    |||:|||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY   225 FLSEPIITFTGAIAFPMPVTIMTI----LYRIYKETERTKELAGLAGSQGEATEENF 280
Db    |||:|||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY   207 ----GSLSRCPSS-----HAGF----- 218
Db    |||:|||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY   281 VHTGSSRSSCSYELOOQSMKRNRKYGRCHFMTTKSWKPSEQMDQHSSSDSNNN 340
Db    |||:|||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY   219 -IATSRSGTGHSRRRTGLACTT-----SLPG----- 242
Db    |||:|||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY   341 DAAASLENASSDEEDIGSETRAIYSIVLKPLPGHSTILNSTKLPSSDNLVPEEELGMVD 400
Db    |||:|||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY   243 LKEPAASLHSES-----PRCKSSLVSIR-----THMSGSI-----IAFKV 278
Db    |||:|||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY   401 LERKADKLQAOKSVDDGGSPFSFKLPIQLAESAVDTAKTSDNVNSVGKSTATLPLSFKE 460
Db    |||:|||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY   279 GS-----FCRSESPVLHOREHVELLRGRLARSIALVLSAFAIWAPYCLFTVLSTVRRG 334
Db    |||:|||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY   461 ATLAKRPALKTRSQITRKREMSLVKEKAQTLSAILAFIITWPYNIMVLV-NTFCDS 519
Db    |||:|||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY   335 ERPKSIWYSIAFWLQFNLSLINPFLPLCHRRRFQKAFKWIL---CVTKQPAPSGTQSVSS 391
Db    |||:|||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY   520 CIPKTFW-NLGWMLCYINSTVNPVCVALCNKTRFTTFKMILLQCQDKKKRKKQQYQQRQS 578
Db    |||:|||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

RESULT 6
A41632
histamine H1 receptor - bovine
C:Species: Bos primigenius taurus (cattle)
C>Date: 28-Aug-1992 #sequence_revision 28-Aug-1992 #text_change 09-Jul-2004
C:Accession: A41632
R:Yamashita, M.; Fukui, H.; Sugama, K.; Horio, Y.; Ito, S.; Mizuguchi, H.; Wada,
Proc. Natl. Acad. Sci. U.S.A. 88, 11515-11519, 1991
A>Title: Expression cloning of a cDNA encoding the bovine histamine H-1 receptor
A:Reference number: A41632; MUID:92107981; PMID:1722337
A:Accession: A41632
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-491 <YAM>
A:Cross-references: UNIPROT:P30546; GB:D10197; GB:D90430; NID:g217569; PIDN:BAA
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match      19.6%; Score 401.5; DB 2; Length 491;
Best Local Similarity 24.8%; Pred. No. 2e-26;
Matches 123; Conservative 82; Mismatches 148; Indels 143; Gaps 18;

QY   1 MSSNGTDLVPLTAQVPLAFLMSLLAFATTIGNAVVILAFVADRNLRHRSNYFFLN 59
Db    |||:|||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY   14 MCQGNKTAPANDAQLTPLVVVLSTISU-VTVGLNLLVLYAVRSERKLUWTGNLVISLSV 72
Db    |||:|||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
```



A: Molecule type: protein  
A: Residues: 104-166 <KUR>  
C: Superfamily: vertebrate rhodopsin  
C: Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; transmembrane  
F: 67-90/Domain: transmembrane #status predicted <TM1>  
F: 104-124/Domain: transmembrane #status predicted <TM2>  
F: 142-163/Domain: transmembrane #status predicted <TM3>  
F: 184-206/Domain: transmembrane #status predicted <TM4>  
F: 230-251/Domain: transmembrane #status predicted <TM5>  
F: 492-512/Domain: transmembrane #status predicted <TM6>  
F: 527-545/Domain: transmembrane #status predicted <TM7>  
F: 6,15,41,48,52/Binding site: carboxydrate (Asn) (covalent) #status predicted

Query Match 19.4%; Score 397.5; DB 2; Length 589;  
Best Local Similarity 24.2%; Pred. No. 5.3e-26;  
Matches 131; Conservative 84; Mismatches 159; Indels 167; Gaps 17;

Qy 4 SNGTDVLPITAQ-----VPLAFLMSLLAFALTIGNAVILAFVADRNLRHRSNYFLNLA 58  
Db 51 SNTSDSPGGHHTIWQVVFIAFTGFLVALVTIIGNILVIVAFKVNKQLTKVNNYFLLSLA 110  
Qy 59 ISDFVGVGISPIYIPIHTLFN-WNPGSGICMFMLITDYLLCTASVYSVLISYDYQSVS 117  
Db 111 CADLIIGVLSMNLFTYYIINRWALGNLACDLWLSIDYVASNASVWNLVLSFDYFYSIT 170  
Qy 118 NAVRYRAQHT----GILKIVAQMVAVMILAFVLPNGPMILASDSW-----KSNSTNTECBP 168  
Db 171 RPLTYRAKRTTKRRGVWIGLA----WVISPVLWAPAIL---FWQYFVGKRTVPVPGECFI 222  
Qy 169 GFVTEWYLLAITAFLEFLPLVSLVYFVSQIYLSWLKR----- 206  
Db 223 QFLSEPTITFTGTAIAAFYMPVTIMTI----LYMRIYKETEKRTKELAGLOASGTEAEAN 278  
Qy 207 -----GSLSRCPSH----AGFIATSSRGTG-----HSRRTGLAC 236  
Db 279 FVHPTGSSRSCSYELQQQGVKSSRRKRYGRCHFVFTKSWKPSAEQMDHSSDSWNN 338  
Qy 237 RTSPLPOLKEPAAS----LHSESPR-----GKSSLVSLRLTHMSGSI----- 273  
Db 339 NDAASAASLENSASSDEEDIGSETRAIYISVLKPLGHSSILNKLKLPSSDLQVSNEDLGTV 398  
Qy 274 ----- 274  
Db 399 DYERNAHKLQAQSMGMDGNCQDFTKLPIQLSEAVDTGKTSDTNSSADKTTATLPLSPK 458  
Qy 278 VGS-----FCRSESPVLHQREHVELLRGKLARSIAVLLSAFACWAPCYCLFIVLSTYRR 333  
Db 459 EATLAKRFALKTRSQITKRGMSLIIEKKAAQTLSAILLAFTITWPNIMVLV-NTPCD 517  
Qy 334 GERPSKIYSIAFWLQFNWLSINPFLYPLCHRRRFQKAFWKIL---CVTKQAPAPSQTSVS 390  
Db 518 SCIPKTYW-NLGWYLCYINSTVNPVCVALCNKTFRTFTFKLLCCQCKRKRKQYQYRQ 576  
Qy 391 S 391  
Db 577 S 577

RESULT 9  
JC2495  
histamine H1 receptor - human  
C: Species: Homo sapiens (man)  
C: Date: 16-Mar-1995 #sequence revision 26-May-1995 #text\_change 09-Jul-2004  
C: Accession: JC2495; J02035; S48144  
R: Fukui, H.; Fujimoto, K.; Mizuguchi, H.; Sakamoto, K.; Horio, Y.; Takai, S.; Yamada, K.  
Biochem. Biophys. Res. Commun. 201, 894-901, 1994  
A: Title: Molecular cloning of the human histamine H1 receptor gene.  
A: Reference number: JC2495; MUID: 94271250; PMID: 8003029  
A: Accession: JC2495  
A: Molecule type: DNA  
A: Residues: 1-487 <RUK>  
A: Cross-references: UNIPROT: P35367; DDBJ: D14436; NID: g506335; PIDN: BAA03319.1; PID: g5382  
R: De Backer, M.D.; Gommeren, W.; Moereels, H.; Nobels, G.; Van Gompel, P.; Leysen, J.E.







C:Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; phospho  
F:25-50/Domain: transmembrane #status predicted <TM1>  
F:62-93/Domain: transmembrane #status predicted <TM2>  
F:100-121/Domain: transmembrane #status predicted <TM3>  
F:142-168/Domain: transmembrane #status predicted <TM4>  
F:187-209/Domain: transmembrane #status predicted <TM5>  
F:367-387/Domain: transmembrane #status predicted <TM6>  
F:402-420/Domain: transmembrane #status predicted <TM7>

Query Match 19.0%; Score 389.5; DB 2; Length 460;  
Best Local Similarity 27.5%; Pred. No. 1.9e-25;  
Matches 119; Conservative 80; Mismatches 161; Indels 73; Gaps 17;

QY 5 NGTDVLPPLTAQVPLAFL---MSLLAFATIGNAVILAFVADRNLRHRSNYFPLNLAISD 61  
DB 12 NITVLAPGPMQVAFIGITGLLSLATVTGNLLVLSFKVNTKLTANNYFLLSLACAD 71  
QY 62 FVGVVISIPLXIPHTLF--NWNPGSGICMFWLITDYLCTASVVISVLISVDRYQSVNAV 120  
DB 72 LIIGTFMNLTYTLMGHWALGTACDLWLADYVNASVNNLLISDFRYFSVTRPL 131  
QY 121 RYRAQHTGILKIVQAVV--WILAFVNGPMILASDSW-----KNSTNTEECPEPGFVTEW 174  
DB 132 SYRAKRP--RRAALMIGLAVSVFVWAPAIL---FWQYLVGERIVLAGQCVIQLSQP 186  
QY 175 YILAITAFLEPLVSLVYVFSQIYVWSLWKR-----GSL--SRCPSHAGFIATSSR 224  
DB 187 IITFTGMAAFYLPVTVM---CTLYWYRYETENRARELAALQGSFPGKGGSSSSSE 242  
QY 225 ---GTGHSRRT--GLACR-TSLPGLKEPAA--SLHSESPRGKSSLLVLRTHMSGIIF 276  
DB 243 RSQPAAGSPETPPGRCRCRPRLLQAYSWKEEEDGSMESLTSSEGEPPGSEVVI 302  
QY 277 KYGSF-CRSESPV-----LHOREHVELLRGRK 302  
DB 303 KPMVDPEAQAPAKQPPRSNPVTKPTRKGRERAGKQKPRGKEQLAKRTFSLVKEK 362  
QY 303 LARSVALLSAFAICWAPYCLFTVLSTYRGERPKSIWYSAFWLQWNSLINPFLYPL 362  
DB 363 AARTLSAILLAFITVTPYINMLV--STFKCKCVPELW--ELGYWLCYVNSTINPWCYAL 420  
QY 363 CHRRQKAFWKIL 375  
DB 421 CNKAFRDTFRLLL 433

RESULT 13  
AS5019  
muscarinic acetylcholine receptor, M3 isoform - chicken  
C:Species: Gallus gallus (chicken)  
C>Date: 11-Nov-1994 #sequence\_revision 11-Nov-1994 #text\_change 09-Jul-2004  
C:Accession: A55019  
R:Gadbut, A.P.; Galper, J.B.  
J. Biol. Chem. 269, 25823-25829, 1994  
A:Title: A novel M-3 muscarinic acetylcholine receptor is expressed in chick atrium and  
A:Reference number: A55019; MUID:95014393; PMID:7929287  
C:Accession: A55019  
A:Status: preliminary  
A:Accession: A55019  
A:Molecule type: mRNA  
A:Residues: 1-639 <C>  
A:Cross-references: UNIPROT:P49578; GB:U10617; NID:G530097; PIDN:AAA65961.1; PID:G530098  
C:Superfamily: vertebrate rhodopsin  
C:Keywords: neurotransmitter receptor

Query Match 19.0%; Score 389; DB 2; Length 639;  
Best Local Similarity 24.8%; Pred. No. 3.1e-25;  
Matches 134; Conservative 89; Mismatches 153; Indels 168; Gaps 21;

QY 2 SBSNGTDVLPPLTAQ-----VPLAFMLSLAFATIGNAVVILAFVADRNLRHRSNYFFLN 56  
DB 98 SSLNATIKDPLGCHAVQVVLIAFLGIALVTIIGNILVIVSFKNQKLTNNYFLLS 157  
QY 57 LAISDFVGVVISIPLXIPHTLF--NWNPGSGICMFWLITDYLCTASVVISVLISYDRYOS 115

DB 158 LACADLIICVISNLTFTTYIINGHWALGNLACDLWLSIDYVNASVMNLLLVISDFRYFS 217  
QY 116 VSNVRYRAQHTGILKIVQAVV--WILAFVNGPMILASDSW-----KNSTNTEECPEG 169  
DB 218 ITRPLTYRAKRT--TKRAGVMIGLAWIISFVLWAPAIL---FWQYFVGKRTVPLDCEFIQ 272  
QY 170 FVTEWYILAITAFLEPLVSLVYVFSQIYVWSLWKRSGLSRCPSHAGFIATSSRG---- 225  
DB 273 FLSEPIITFTGTAIAAFYLPVTIM---SI-LYWRYIYKE--TEKRTKELAGLQASGSEABTAR 327  
QY 226 ----TCHSRRTG-----LACRTSLPGL----- 243  
DB 328 FVHTGSSSLSSLYELQROSTRSSRRKRYRCHFWLTMTKSWSPNTDQGOEHSSSSWNN 387  
QY 244 KPPAASLHSES-----PRGKSSLLVLRTHMSGIIFKV----- 278  
DB 388 NDAASLANSASDEEDITAEITRAIYIVLKLPGH--SAILNSTKLPSSEDLNESADELQK 446  
QY 279 -----GSPCRSES--PV----- 288  
DB 447 SDTDSOEKPKKLQPPKSIQDGSFQKPSKLPQPSAETATASDGISSVTKTSAALPL 506  
QY 289 -----LHOREHVELLRGRKLARSILAVLSAFAICWAPYCLFTVLST 330  
DB 507 SPKEATLAKKFAKTRSQITTKRMSLIKEKAAQOTLSAILFAFIITWTPYINMLV--NT 565  
QY 331 YRGERPKSIWYSAFWLQWNSLINPFLYPLCHRRFQKAFWKIL---CVTKOPAPSQTQ 387  
DB 566 FDCV-PKTVW--NLGWLCYINSTVNPVCYALCNKMFRTFMILLCCQCKRKRKQOYQ 623  
QY 388 SVSS 391  
DB 624 QROS 627

RESULT 14  
S09508  
muscarinic acetylcholine receptor M1 - human  
C:Species: Homo sapiens (man)  
C>Date: 31-Dec-1990 #sequence\_revision 31-Dec-1990 #text\_change 09-Jul-2004  
C:Accession: S09508; S06327; S04326  
R:Chapman, C.G.; Browne, M.J.  
Nucleic Acids Res. 18, 2191, 1990  
A:Title: Isolation of the human m1 (Hml) muscarinic acetylcholine receptor gene by PCR an  
A:Reference number: S09508; MUID:90245684; PMID:2336407  
A:Accession: S09508  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-460 <CHA>  
A:Cross-references: UNIPROT:P11229; EMBL:X52068; NID:G34450; PIDN:CAA36291.1; PID:G34451  
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, March 1990  
R:Allard, W.J.; Sigal, I.S.; Dixon, R.A.F.  
Nucleic Acids Res. 15, 10804, 1987  
A:Title: Sequence of the gene encoding the human M1 muscarinic acetylcholine receptor.  
A:Reference number: S06327; MUID:88096607; PMID:3697105  
A:Accession: S06327  
A:Molecule type: DNA  
A:Residues: 1-460 <ALL>  
A:Cross-references: GB:Y00508; GB:M35128; NID:G297405; PIDN:CAA68560.1; PID:G297406  
R:Peralta, E.G.; Ashkenazi, A.; Winslow, J.W.; Smith, D.H.; Ramchandran, J.; Capon, D.J.  
EMBO J. 6, 3923-3929, 1987  
A:Title: Distinct primary structures, ligand-binding properties and tissue-specific expre  
A:Reference number: S04326; MUID:88166632; PMID:3443095  
A:Accession: S04326  
A:Molecule type: DNA  
A:Residues: 1-172, 'M', 174-460 <PER>  
A:Cross-references: EMBL:X15263; NID:G32317; PIDN:CAA33334.1; PID:G32318  
C:Superfamily: vertebrate rhodopsin  
C:Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; phospho  
F:25-50/Domain: transmembrane #status predicted <TM1>  
F:62-93/Domain: transmembrane #status predicted <TM2>  
F:100-121/Domain: transmembrane #status predicted <TM3>



GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: August 5, 2005, 13:53:45 ; Search time 3173 Seconds  
(without alignments)  
4690.554 Million cell updates/sec

Title: US-10-626-126-9

Perfect score: 2045

Sequence: 1 MSESNGTDLPLTAQVPLAF.....WKILCVTKQAPSPQSVSS 391

Scoring table:

BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlp  
-Q=/cpn2.1/USPTO.spool\_p/US10626126/runat\_02082005\_155436\_2017/app.query.fasta\_1.583  
-DB=EST -QFMT=fastap -SUFFIX=rest -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US10626126 @CN 1 1 5180 @runat\_02082005\_155436\_2017 -NCPU=3  
-NO MAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -XGAPOP=10 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST: \*  
1: gb\_est1: \*  
2: gb\_est2: \*  
3: gb\_hic: \*  
4: gb\_est3: \*  
5: gb\_est4: \*  
6: gb\_est5: \*  
7: gb\_est6: \*  
8: gb\_gss1: \*  
9: gb\_gss2: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	875	42.8	839	5 BX643713	BX643713 DKFZp781C
2	857	41.9	704	7 CF147821	CF147821 AGENCOURT
3	484	23.7	721	7 CO959034	CO959034 AGENCOURT
4	456.5	22.3	732	7 CF147822	CF147822 AGENCOURT
5	405	19.6	1773	9 AY400782	AY400782 Homo sapi
6	401	19.6	672	6 CB556920	CB556920 AMGNNUC:U
7	397.5	19.4	853	6 CD326085	CD326085 AGENCOURT
8	397.5	19.4	1770	9 AY400784	AY400784 Mus muscu
9	397.5	19.4	3171	3 AK080950	AK080950 Mus muscu

10	392.5	19.2	2780	3 AK032763	AK032763 Mus muscu
11	392.5	19.2	2831	3 AK047070	AK047070 Mus muscu
12	392.5	19.2	2979	3 AK038480	AK038480 Mus muscu
13	392.5	19.2	3783	3 AK046607	AK046607 Mus muscu
14	390.5	19.1	1161	9 AY415607	AY415607 Mus muscu
15	387.5	18.9	1173	9 AY415605	AY415605 Homo sapi
16	384	18.8	3816	3 AK081248	AK081248 Mus muscu
17	380.5	18.6	1173	9 AY415606	AY415606 Pan trogl
18	372.5	18.2	1764	3 BC018330	BC018330 Mus muscu
19	372.5	18.2	2611	3 AK004891	AK004891 Mus muscu
20	372.5	18.2	3050	3 AK043877	AK043877 Mus muscu
21	365.5	17.9	1401	9 AY399426	AY399426 Homo sapi
22	359	17.6	1134	9 AY418218	AY418218 Homo sapi
23	358.5	17.5	1440	9 AY404936	AY404936 Mus muscu
24	358.5	17.5	2578	3 AK045364	AK045364 Mus muscu
25	357.5	17.5	2232	3 CR606112	CR606112 full-leng
26	356.5	17.4	1125	9 AY418220	AY418220 Mus muscu
27	356.5	17.4	2908	3 AK082016	AK082016 Mus muscu
28	354.5	17.3	1440	9 AY404935	AY404935 Pan trogl
29	352.5	17.2	1203	9 AY407499	AY407499 Homo sapi
30	352.5	17.2	1440	9 AY404934	AY404934 Homo sapi
31	351.5	17.2	1072	9 AY398880	AY398880 Homo sapi
32	351.5	17.2	1401	9 AY399428	AY399428 Mus muscu
33	351.5	17.2	4124	3 AK085653	AK085653 Mus muscu
34	351.5	17.2	4135	3 AK079597	AK079597 Mus muscu
35	347.5	17.0	1072	9 AY398881	AY398881 Pan trogl
36	343.5	16.8	1203	9 AY407500	AY407500 Pan trogl
37	340.5	16.7	1069	9 AY398882	AY398882 Mus muscu
38	337.5	16.5	2410	3 BC035047	BC035047 Homo sapi
39	334.5	16.4	3594	3 AK046802	AK046802 Mus muscu
40	333.5	16.3	1335	9 AY418853	AY418853 Mus muscu
41	333.5	16.3	1347	9 AY416858	AY416858 Mus muscu
42	330	16.1	1200	9 AY407501	AY407501 Mus muscu
43	328.5	16.1	1353	9 AY416856	AY416856 Homo sapi
44	326.5	16.0	1269	9 AY402237	AY402237 Homo sapi
45	322.5	15.8	1269	9 AY402239	AY402239 Mus muscu

#### ALIGNMENTS

RESULT 1

LOCUS BX643713

DEFINITION DKFZp781C0629\_1

839 bp mRNA linear EST 04-SEP-2003

DKFZp781C0629 5', mRNA sequence.

ACCESSION BX643713

VERSION BX643713.1

KEYWORDS GI:34478046

SOURCE EST.

ORGANISM Homo sapiens (human)

REFERENCE 1 (bases 1 to 839)

AUTHORS Lauber,J., Bahr,A., Mewes,H.W., Weil,B., Amid,C., Oeanger,A.,

Fobo,G., Han,M. and Wiemann,S.

EST (Lauber,J., Bahr,A., Mewes,H.W., Weil,B., Amid,C., et al.)

JOURNAL Unpublished (2003)

COMMENT Contact: MIPS

MIPS

Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany

This is the 5' sequence of the clone insert

Clone from S. Wiemann, Molecular Genome Analysis, German Cancer

Research Center (DKFZ); Email: s.wiemann@dkfz-heidelberg.de;

sequenced by Olagen (Hilden/Germany) within the CDNA sequencing

consortium of the German Genome Project.

No sl sequence available.

This clone (DKFZp781C0629) is available at the RZPD in Berlin.

Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059

Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES

source

1..839

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"  
/clone="DKFZp781C0629"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/clone\_lib="781 (synonym: hicc4)"  
/note="Vector: pSport1\_Sfi; Site\_1: SfiIA; Site\_2: SfiIB;  
cDNA-collection"

## ORIGIN

## Alignment Scores:

Pred. No.: 9,65e-76 Length: 839  
Score: 875.00 Matches: 175  
Percent Similarity: 79.92% Conservative: 24  
Best Local Similarity: 70.26% Mismatches: 48  
Query Match: 42.73% Indels: 3  
DB: 5 Gaps: 1

US-10-626-126-9 (1-391) x BX643713 (1-839)

```
QY 1 MetSerGluSerAsnGlyThrAspValLeuProLeuThrAlaGlnValProLeuAlaPhe 20
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
96 ATGCCAGATACATAAGACAAATCAATTTATCCTAAGCACTCGTGTACTTTAGCATTT 155
QY 21 LeuMetSerLeuLeuAlaPheAlaIleThrIleGlyAsnAlaValIleLeuAlaPhe 40
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
156 TTTATGCTCTTAGTAGCTTTGCTATATGCTAGGAATGCTTTGCTCATTTAGCTTTT 215
QY 41 ValAlaAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
216 GTGGTGGACAAACCTAGACATCGAAGTAGTTATTTTCTTAACCTGGCCATCTCT 275
QY 61 AspPhePheValGlyValIleSerIleProLeuTyrIleProHisThrLeuPheAsnTrp 80
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
276 GACTCTTTGTGGGTGATCTCCATCTTTGTATCATCCCTCACAGCTGTGGAATGG 335
QY 81 AsnProGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeuLeuCysThrAla 100
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
336 GATTTTGGAAAGGAATCTGTGATTTTGGCTCACTACTGACTATCTGTATGTACGCA 395
QY 101 SerValTyrSerIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
396 TCTGTATATAACATGTCTCATCATCATGATGATGATGATGATGATGATGATGATGAT 455
QY 121 ArgTyrArgAlaGlnHisThrGlyIleLeuValIleValAlaGlnMetValAlaValTrp 140
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
456 TCTTATAGAACTCAACATCACTGGGTCTTTGAAGATTGTACTCTGATGGTGGCCGTTGG 515
QY 141 IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTrpIlyAsnSer 160
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
516 GTGCTGGCTCTTAGTGAATGGCCCAATGATCTCTAGTTTCAGAGCTCTTGGAGGATGA 575
QY 161 ThrAsnThrGluGluCysGluProGlyPheValThrGluTyrTyrIleLeuAlaIleThr 180
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
576 GGTAGT-----GAATGTGAACCTGGATTTTTCGGAATGGTACATCTCCATCCATCA 629
QY 181 AlaPheLeuGluPheLeuLeuProValSerLeuValValTyrPheSerValGlnIleTyr 200
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
630 TCATCTTGGAAATCTGTGATCCAGTCATCTTAGTGGCTTATTTCAACATGAATATTAT 689
QY 201 TrpSerLeuTrpLysArgGlySerLeuSerArgCysProSerHisAlaGlyPheIleAla 220
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
690 TGGAGCTGTGGAGGTGATCATCTCAGTAGTGGCCAAAGCCATCTCGACTGCTGCT 749
QY 221 ThrSerSerArgGlyThrGlyHisSerArgArgThrGlyLeuAlaCysArgThrSerLeu 240
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
750 GTCCTCTCCACATCTGT-GGACACTCAATTCAGAGGTAGACTATCTTCAAGGAGATCTCT 808
QY 241 ProGlyLeuLysGluProAlaAlaSer 249
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
809 TCTGCATCGACAGAAGTCTCCTGCATCC 835
```

RESULT 2  
,CF147821

LOCUS CF147821 704 bp mRNA linear EST 25-JUL-2003  
DEFINITION AGENCOURT 14740195 NIH\_MGC\_145 Homo sapiens cDNA clone  
IMAGE:6971900 5', mRNA sequence.  
ACCESSION CF147821  
VERSION CF147821.1 GI:33244089  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 704)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Daniela S. Gerhard, Ph.D.  
Office of Cancer Genomics  
National Cancer Institute / NIH  
Bldg. 31 Rm10A07 Bethesda, MD 20892  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: GPCR Consortium  
cDNA Library Preparation: GPCR Consortium  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: IRS102 row: B column: 07  
High quality sequence stop: 685.  
Location/Qualifiers  
1..704  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:6971900"  
/tissue\_type="mixed"  
/lab\_host="DH10B"  
/clone\_lib="NIH\_MGC\_145"  
/note="Vector: pCDNA3.1; Site 1: varies by clone; Site 2:  
varies by clone; ORFs were PCR-amplified and cloned into  
pCDNA3.1 by the GPCR Consortium. Cloning sites vary by  
clone and include the following: 5'-EcoRV-XmiI/XhoI-3',  
5'-EcoRV-XmiI/NotI-3', EcoRV (TA cloned, non-directional).  
For information about which gene each clones represents,  
please visit our anonymous ftp site at  
ftp://image.llnl.gov/image/rearranged\_plates/IRBI.presv.dat  
a Note: this is a NIH\_MGC Library."

## ORIGIN

## Alignment Scores:

Pred. No.: 4,4e-74 Length: 704  
Score: 857.00 Matches: 169  
Percent Similarity: 82.13% Conservative: 24  
Best Local Similarity: 71.91% Mismatches: 40  
Query Match: 41.91% Indels: 3  
DB: 7 Gaps: 1

US-10-626-126-9 (1-391) x CF147821 (1-704)

```
QY 3 GluSerAsnGlyThrAspValLeuProLeuThrAlaGlnValProLeuAlaPheLeuMet 22
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
5 GATACATATAGCACATCAATTTATCCTAAGCACTCGTGTACTTTAGCATTTTATG 64
QY 23 SerLeuLeuAlaPheAlaIleThrIleGlyAsnAlaValIleLeuAlaPheValAla 42
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
65 TCCTTAGTAGCTTTTGGCTATATGCTAGGAATGCTTTGGTTCATTTAGCTTTTGGTGG 124
QY 43 AspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSerAspPhe 62
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
125 GACAAAACCTTAGACATCGAAGTAGTTATTTTCTTAACCTGGCCATCTCTGACTTC 184
QY 63 PheValGlyValIleSerIleProLeuTyrIleProHisThrLeuPheAsnTrpAsnPro 82
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
185 TTTGTGGGTGTGATCTCCATTCCTTTGTACATCCCTCACACGCTTCGAATGGGATTTT 244
```



DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>

Plate: IRB102 row: b column: 06

High quality sequence stop: 610.

Location/Qualifiers

1..732

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:6971899"

/tissue\_type="mixed"

/lab\_host="DH10B"

/clone\_lib="NIH\_MGC\_145"

/notes="Vector: pCDNA3.1; Site 1: varies by clone; Site 2:  
varies by clone; ORFs were PCR-amplified and cloned into  
pCDNA3.1 by the GPCR Consortium. Cloning sites vary by  
clone and include the following: 5'-EcoRV-XmnI/XhoI-3',  
5'-EcoRV-XmnI/NotI-3', EcoRV (TA cloned, non-directional).  
For information about which gene each clone represents,  
please visit our anonymous ftp site at  
[ftp://image.llnl.gov/image/rearranged\\_plates/IRB1.presv.dat](ftp://image.llnl.gov/image/rearranged_plates/IRB1.presv.dat)  
a Note: this is a NIH\_MGC Library."

## ORIGIN

Alignment Scores:  
Pred. No.: 2.17e-34 Length: 732  
Score: 456.50 Matches: 95  
Percent Similarity: 64.47% Conservative: 32  
Best Local Similarity: 48.22% Mismatches: 59  
Query Match: 22.32% Indels: 11  
DB: 7 Gaps: 4

US-10-626-126-9 (1-391) x CF147822 (1-732)

Qy 18 LeuAlaPheLeuMetSerLeuAlaPheAlaThrIleGlyAsnAlaValIle 37  
Db 125 CTGGCGGCTCATYGGCGCTGCTCATCTGCGCCAGCGTGTGGGCAACGCGTGTGATG 184  
Qy 38 LeuAlaPheValAlaAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeu 57  
Db 185 CTCGCTTCTGTGGCGCATCGAGCGCTCGACCCAGAACAACTTCTTCTGCTCAACCTC 244  
Qy 58 AlaIleSerAspPheValGlyValIleSerIleProLeuTyrIleProHisThrLeu 77  
Db 245 GCCATCTCCGACTTCTCTGTCGGCGCCCTTGTGATCCCACTGTATGTACCTACGTGCTG 304  
Qy 78 Phe---AsnTyrAsnProGlySerGlyIleCysMetPheThrLeuIleThrAspTyrLeu 96  
Db 305 ACAGGCGCTGGACCTTTCGGCGGGGCTCTGCAAGCTGTGGTGTGTGACTTACCTG 364  
Qy 97 LeuCysThrAlaSerValTyrSerIleValLeuIleSerTyrAspArgTyrGlnSerVal 116  
Db 365 CTGTGCACCTCTCTGCTTCAACATCTGTCTCATCTAGTACGACCGCTTCTGTCGGTCT 424  
Qy 117 SerAsnAlaValArgTyrArgAlaGlnHisThrGlyIleLeuLysIleValAlaGlnMet 136  
Db 425 ACCGAGCGGTCTCATACCGGGCCCGACGAGGTGACACGCGCGGGCGGTGCGGAGATG 484  
Qy 137 ValAlaValTyrIleLeuAlaPheLeuValAlaGlyProMetIleLeuAlaSerAspSer 156  
Db 485 CTGCTGGTGTGGTGTGGCTTCTGCTGTACGAGCAGCCATCTCTG-----AGC 535  
Qy 157 TrpLys-----AsnSerThrAsnThrGluGluCysGluProGlyPheVal 171  
Db 536 TGGAGTACCTGTCCGGGGGAGCTCCATCCCGAGGGCCACTGTATGCCAGTCTTC 595  
Qy 172 ThrGluTyrTyrIleLeuAlaIleThrAlaPheLeuGluPheLeuProValSerLeu 191  
Db 596 TACAACTGTCTTCTTTCATCAGCGCTTCCACACGTGGAGTCTTTACCGCCCTCTCAGC 655  
Qy 192 ValValTyrPheSerValGlnIleTyrTrpSerLeuTyrLysArgGlySer 208

Db 656 GTCACTTCTTAACCTCACCATTCTACTGAAATC-----AGAGGGCA 700

RESULT 5  
AY400782

## LOCUS

## DEFINITION

AY400782

AY400782.1 GI:39756771

GSS.

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

1 (bases 1 to 1773)

Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A.,

Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,

Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,

Adams, M.D. and Cargill, M.

Inferring nonneutral evolution from human-chimp-mouse orthologous

gene trios

Science 302 (5652), 1960-1963 (2003)

14671302

2 (bases 1 to 1773)

Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A.,

Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,

Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,

Adams, M.D. and Cargill, M.

Direct Submission

Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,

Rockville, MD 20850, USA

This sequence was made by sequencing genomic exons and ordering

them based on alignment.

Location/Qualifiers

1..1773

/organism="Homo sapiens"

/mol\_type="genomic DNA"

/db\_xref="taxon:9606"

<1..>1773

/gene="CHRM3"

/locus\_tag="HCM0672"

## ORIGIN

## Alignment Scores:

Pred. No.: 1.16e-28 Length: 1773  
Score: 405.00 Matches: 141  
Percent Similarity: 41.71% Conservative: 83  
Best Local Similarity: 26.26% Mismatches: 159  
Query Match: 19.80% Indels: 155  
DB: 9 Gaps: 19

US-10-626-126-9 (1-391) x AY400782 (1-1773)

Qy 2 SerGluSerAsnGlyThrAspValLeuProLeuThrAlaGln-----Val 16  
Db 148 TCTCTCCAGACGGTACCCAGCATGACCTCTGGAGGTGCATACCGTCTGGCAAGTGTG 207  
Qy 17 ProLeuAlaPheLeuMetSerLeuLeuAlaPheAlaIleThrIleGlyAsnAlaVal 36  
Db 208 TTCATCGCTTTCTTAAACGGGCATCTGCGCTTGTGTGACCATCATCGGCAACATCCTG 267  
Qy 37 IleLeuAlaPheValAlaAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeu 56  
Db 268 ATTGTGTCATTAAAGGTCAACAGCAGCTGAAGACGGTCAACAACTACTTCTCTTAAGC 327  
Qy 57 LeuAlaIleSerAspPhePheValGlyValIleSerIleProLeuTyrIleProHisThr 76  
Db 328 CTGGCTGTGGCGATCTGATTATCGGGTCTATTCAATGATCTGTTACGACCTACATC 387  
Qy 77 LeuPheAsn---TrpAsnProGlySerGlyIleCysMetPheThrLeuIleThrAspTyr 95  
Db 388 ATCATGAATCGATGGCGCTTAGGGAACCTGGCGCTGTGACCTCTGGCTTGCCATTGACTAC 447

Qy	96	LeuLeuCysThrAlaSerValTyrSerIleValLeuIleSerTyrAspArgTyrGlnSer	115
Db	448	GTAGCCAGCAATGCCTGTGTATGAATCTTCTGGTCATCAGCTTGTGACAGATACTTTTCC	507
Qy	116	ValSerAsnAlaValArgTyrArgAlaGlnHisThrGlyIleLeuValIleValAlaGln	135
Db	508	ATCAGAGCGCGCTCAGTACCGGACGCCAAGCAAGCA-----ACAAAGAGAGCGCGGTGTG	561
Qy	136	MetValAlaVal---TrpIleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSer	154
Db	562	ATGATCGGTCTGGCTTGGGTGCATCTCCTTTGTCTTTTGGGCTCCTGCCATCTTG-----	615
Qy	155	AspSerTrp-----LysAsnSerThrAsnThrGluGluCysGluProGly	169
Db	616	---TTCTGGCAATACTTTTGTGGAAAGAGAACTGTGCTCCGGGAGAGTGTCTTATTCAG	672
Qy	170	PheValThrGluTrpTyrIleLeuAlaIleThrAlaPheLeuGluPheLeuProVal	189
Db	673	TTCTCAGTGAAGCCCACTTACTTTTGGCAGCCCATCGCTGCTTTTATATGCGCTGTG	732
Qy	190	SerLeuValValTyrPheSerValGln-----	198
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Qy	199	IleTyrTrp-----SerLeuTrpLysArgGly---SerLeuSerArgCysProSerHis	215
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Qy	249	SerLeuHisSerGluSerProArgGlyLys-SerSerLeuLeuValSerLeuArgThrHi	268
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Db	1569	AACCTTTTGG---AAYCTGGGCTACTGGCTGTGCTATCATCAACGACCGTGAAACCCCGT	1625
Qy	358	eLeuTyrProLeuCysHisArgPheGlnTysAlaPheTyrPheIleLeu-Cys----	376
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Qy	377	--ValThrTysGlnProAlaProSerClnThrGlnSerValSerSer	391
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DEFINITION	AMGNNUC:URGP1-00001-D6-A urgp1 (14349) Rattus norvegicus cDNA clone		
ACCESSION	urgp1-00001-d6 5', mRNA sequence.		
VERSION	CB556920		
KEYWORDS	CB556920.1 GI:29496320		
SOURCE	EST.		
ORGANISM	Rattus norvegicus (Norway rat)		
REFERENCE	1 (bases 1 to 672)		
AUTHORS	Angen EST Program.		
TITLE	Angen Rat EST Program		
JOURNAL	Unpublished (2003)		
COMMENT	Contact: Dan Fitzpatrick		
	Angen, Inc		
	One Angen Center Drive, Thousand Oaks, CA 91320-1799, USA		
	Tel: 805 447-4881		
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Pred. No.:	5,93e-29	Length:	672
Score:	401.00	Matches:	80
Percent Similarity:	71.83%	Conservative:	22
Best Local Similarity:	56.34%	Mismatches:	36
Query Match:	19.61%	Indels:	4
DB:	6	Gaps:	2
US-10-626-126-9 (1-391) x CB556920 (1-672)			
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Db	227	CTGGCTCGGCTCATGGCGCTGCTCATCTGGCCACAGTACTGGGCAACGCGTGGTTCATG	286
Qy	38	LeuAlaPheValAlaAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeu	57
Db	287	CTCCGCTTCGTGGCGGATTCCAGCCCTCCGACCCGAGAACCACTCTTCTTGCTCAACCTC	346
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Db	347	GCCATCTCCGAACTTCCTGGTGGGTGGCTTCTGTCATCCCATGTACGTACCTATGTGCTG	406
Qy	78	Phe---AsnTyrAsnProGlySerGlyIleCysMetPheTyrPheLeuIleThrAspTyrLeu	96



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Qy 117 SerAenAlaValArGtyrArGaLagLnHisThrGlyIleLeuLyIleValAlaGlnMet 136  
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Qy 137 ValAlaValTrpIleLeuAlaPhseuValangGlyProMetIleLeuAlaSerAspSer 156  
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Qy 157 TrpLys 158  
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Db 638 TGGAG 643

RESULT 7  
CD326085                    853 bp       mRNA       linear   EST 28-MAY-2003  
LOCUS                      AGENCOURT\_14163426\_NICHDXGC\_Eyel Xenopus laevis cDNA clone  
DEFINITION IMAGE:6949081.5', mRNA sequence.  
CD326085  
CD326085.1 GI:31090416  
EST.  
Xenopus laevis (African clawed frog)  
Xenopus laevis  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;  
Xenopodinae; Xenopus; Xenopus.  
1 (bases 1 to 853)  
NTH-MGC http://mgc.nci.nih.gov/  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Daniela S. Gerhard, Ph.D.  
Office of Cancer Genomics  
National Cancer Institute / NIH  
Bldg. 31 Rm10A07 Bethesda, MD 20892  
Email: cgapob-re@mail.nih.gov  
Tissue Procurement:  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLAMA14564 Row: f Column: 24  
High quality sequence stop: 707.

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Average insert size 2.3 kb. Constructed by Life  
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(XGC) library."

ORIGIN

Alignment Scores:  
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Percent Similarity: 70.13% Conservative: 27  
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Query Match: 19.44% Indels: 5  
DB: 6 Gaps: 2

## ORIGIN

## Alignment Scores:

Pred. No.: 6,39e-28 Length: 1770  
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 Query Match: 19,44% Indels: 155  
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US-10-626-126-9 (1-391) x AY400784 (1-1770)

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 DB 151 TCAATTAAGTCAACAAACAGCTGAAGACAGTCAACAACTACTTCTTTAAGCGCTGGCC 330  
 QY 19 AlaPheLeuMetSerLeuLeuAlaPheAlaIleThrIleGlyAsnAlaValAlaLeu 38  
 DB 211 GCATTTCTGACTGGCTTCTGGCATTTGGTGACCATCATCGGCAACATCCTTTGTCAATGTG 270  
 QY 39 AlaPheValAlaAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAla 58  
 DB 271 GCATTTAAGTCAACAAACAGCTGAAGACAGTCAACAACTACTTCTTTAAGCGCTGGCC 330  
 QY 59 IleSerAspPheValGlyValIleSerIleProLeuTyrIleProHisThrLeuPhe 78  
 DB 331 TGGCGAGATCTGATCATCTGGGGTCAITTTCCATGAACCTGTTCCAGACCTACATCATATG 390  
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 QY 172 ThrGluTrpTyrIleLeuAlaIleThrAlaPheLeuGluPheLeuProValSerLeu 191  
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 Mus musculus (house mouse)  
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 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE  
 1  
 AUTHORS  
 TITLE  
 JOURNAL  
 MEDLINE  
 PUBMED  
 REFERENCE  
 2  
 AUTHORS  
 TITLE  
 JOURNAL  
 MEDLINE  
 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,  
 Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
 Normalization and subtraction of cap-trapper-selected cDNAs to  
 prepare full-length cDNA libraries for rapid discovery of new genes  
 Genome Res. 10 (10), 1617-1630 (2000)  
 20499374

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11042159
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REFERENCE
AUTHORS
Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
Kono,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
Sum,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
Fujiwaka,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
Yoneda,Y., Iehikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
20530913
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11076861
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AUTHORS
The RIKEN Genome Exploration Research Group Phase II Team and the
FANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
5
The FANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 3171)
Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,
Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,
Kato,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
Koya,S., Kurihara,C., Matsuura,T., Miyazaki,A., Murata,M.,
Nakamura,M., Nishi,K., Nomura,K., Nunazaki,R., Ohno,M., Ohsato,N.,
Okazaki,Y., Saito,K., Saichou,H., Sakai,C., Sakai,K., Sakazume,N.,
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Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
Muramatsu,M. and Hayashizaki,Y.
Direct Submission
Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp,
URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
Fax:81-45-503-9216)
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/
FEATURES
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Query Match: 19.44% Indels: 155
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US-10-626-126-9 (1-391) x AK080950 (1-3171)
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1460 AGTGAGCCCACTCACCTTCGGCAGCGGATCGCTGCTTTTACATGCTGCTCACCATC 1519
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Qy 192 ValValTyrPheSerValGln-----LysAsnSerThrAsnThrGluGluCysGluProGlyPheVal 171
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1520 ATGAC-TATTTTATCTAGGAATCTATAAGAGAGACTGAGAAACGTACCAAGAGCTGGC 1578
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Qy 201 TrpSer-----LeuTrpLysArg---GlySerLeuSerArgCysProSerHisAlaGly 217

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Db 1579 TGGGCTACAGGCTCTGGGACAGCGGAAGCAGAAAATTTGTCCACCCACAGGCAG 1638  
Qy 218 Pheile-----AlaThrSerSerArg-GlyThrGlyHisSerArgAr 231  
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Qy 231 gThrGlyLeuAlaCys-----ArgThrSerLeuProGlyLeuLys-- 244  
Db 1699 GAAGTATGGTGGTGTCTCACTTCTGTTTCAACAATAAGAGCTGGAAGCCAGTCTGACGA 1758  
Qy 245 -----GluProAlaAlaSerLe 250  
Db 1759 GATGGACCAAGACCAAGTAGCAGTACAGTGTGAATAACAACGATGCTGCTCCCTCCCT 1818  
Qy 250 uHisSerGluSerProArg----- 256  
Db 1819 GGAATACTGCTCTTCTGATGAGGATATTTGGTCTCAGACCCAGAGCCATCTATTTC 1878  
Qy 257 -----GlyLysSerSerLeuLeuValSerLeuArgThrHisMetSe 270  
Db 1879 CATTTGACTCAAGCTGCGGGTCTATAGCACCATCTCAACTCTACCAAGCTACCCCTCCTC 1938  
Qy 270 rGlySerIle----- 273  
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Qy 273 ----- 273  
Db 2059 GCTCCCATCCAGTTAGAGTCTGCGTGGACAGCAAGCACTCTGACACCAACTCCTC 2118  
Qy 274 -----IleAlaPheLysValGlySer----- 280  
Db 2119 GGTGGACAAGACACGCGCGCTTACTCTGCTCTTCAAGAAGACCGCTGGCTAAGAG 2178  
Qy 281 -PheCysArgSerGluSerProValLeuHisGlnArgGluHisValGluLeuLeuArgG1 300  
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Db 2299 CTACAACATCATCGTCTGGTG---AACACCTTCTGTGACAGCTGCATACCCAAAACCTA 2355  
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Qy 360 rProLeuCysHisArgPheGlnLysAlaPheTrpLysIleLeu-----CysVa 377  
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Qy 377 lThrLysGlnProAlaProSerGlnThrGlnSerValSerSer 391  
Db 2473 CAAGAGGAGCGCGCAACAGCAGTACCAAGCAGACAGTCC 2515

RESULT 10  
LOCUS AK032763  
DEFINITION Mus musculus 12 days embryo male wolffian duct includes surrounding region cDNA, RIKEN full-length enriched library, clone:6720430L06  
product:HISTAMINE RECEPTOR H1, full insert sequence.  
ACCESSION AK032763  
VERSION AK032763.1 GI:26328544  
KEYWORDS HTC; CAP trapper.  
SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus  
REFERENCE 1  
AUTHORS Carninci, P. and Hayashizaki, Y.  
TITLE High-efficiency full-length cDNA cloning  
JOURNAL Meth. Enzymol. 303, 19-44 (1999)  
MEDLINE 99279253  
PUBMED 10349636  
REFERENCE 2  
AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes  
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)  
MEDLINE 20499374  
PUBMED 11042159  
REFERENCE 3  
AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsumai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.  
TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer  
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)  
MEDLINE 20530913  
PUBMED 11076861  
REFERENCE 4  
AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.  
TITLE Functional annotation of a full-length mouse cDNA collection  
JOURNAL Nature 409, 685-690 (2001)  
REFERENCE 5  
AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.  
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs  
JOURNAL Nature 420, 563-573 (2002)  
REFERENCE 6  
AUTHORS Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Iotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.  
TITLE Direct Submission  
JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration and Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gs.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)  
COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.  
Please visit our web site for further details.  
URL: http://genome.gsc.riken.jp/  
URL: http://fantom.gsc.riken.jp/  
Location/Qualifiers  
1. .2780  
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```

CDS

## ORIGIN

## Alignment Scores:

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Pred. No.: 4,18e-27 Length: 2780
Score: 392.50 Matches: 126
Percent Similarity: 42.74% Conservative: 80
Best Local Similarity: 26.14% Mismatches: 159
Query Match: 19.19% Indels: 118
DB: 3 Gaps: 18

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US-10-626-126-9 (1-391) x AK032763 (1-2780)

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QY 1 MetSerGluSerAsnGlyThrAspValLeuProLeuThrAlaGlnValProLeuAlaPhe 20
DB 109 ATGTGTGAGGGGAACAGGACA---GCCATGGCCAGCCCTCAGCTGTCGCCCTGGTGGTG 165
QY 21 LeuMetSerLeuLeuAlaPheAlaIleThrIleGly---AsnAlaValValIleLeuAla 39
DB 166 GTTCTAAGTAGTATCTCCCTG---GTCACAGTGGGCGCTCAACTGCTGTGCTGTATGCA 222
QY 40 PheValAlaAspAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIle 59
DB 223 GTGGCAGTGAGGCAAGCTACACACCGTGGGCAACCTGTACATTGTGACGCTGTCGGTA 282
QY 60 SerAspPheValGlyValIleSerIleProLeuTyrIleProHisThrLeuPhe--- 78
DB 283 GCAGACCTGATTGTAGGGCAGTCGTGATGCCCATCAACATCTCTATCTATCATGACC 342
QY 79 AsnTyrAsnProGlySerGlyIleCysMetPheTyrLeuIleThrAspTyrLeuLeuCys 98
DB 343 AAGTGGTCCCTGGCGCCGCTCTGCTCTTTGGCTCTCTATGATTATGTGGCCAGC 402
QY 99 ThrAlaSerValTyrSerIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsn 118
DB 403 ACGGCATCCATCTTTAGTGTCTTCATCTGTGATTGATCGTACCGCTCTGTCCAGCAA 462
QY 119 AlaValArgTyrArgAlaGlnHisThrGlyIleLeuLeuIleValAlaGlnMetValAla 138
DB 463 CCCTCCGGTACTGAGGTATGCAACCAAG---ACCCGTGCTTCAGCTACCATCTCTGGG 519
QY 139 ValTyrIleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTyrPlys 158
DB 520 GCCTGGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 567
QY 159 AsnSerThr-----AenThrGluGluCysGluProGlyPheValThr 172
DB 568 CACTTCACGCCCTGGCCCCAGAGCTTCGGGAAGATAAGTGTGAGACAGATTCTACAAAT 627

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QY 173 GluTyrTyrIleLeuAlaIleThrAlaPheLeuGluPheLeuLeuProValSerLeuVal 192
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QY 193 ValTyrPheSerValGlnIleTyr----- 200
DB 688 CTGTGGTTCTATGTGAAGATCTTACAAAGCTGTGGGGCAGACTGTTCAGCACCAGCCAGCTC 747
QY 200 ----- 200
DB 748 ACCAACGGGTCCCTCCCTACCTCTTTTAAAGATCAAGCTGAGTCCGAGGATGCCAAAGAG 807
QY 201 -----TyrSerLeuTyrPlysArg----- 206
DB 808 GGTGCAAGAAACCTGGGAAAGAGTCTCCCTGGGGGGTCCAGAGAGAGCGGTCACAGAGAC 867
QY 207 -----GlySerLeuSerArgCysProSerHisAlaGly-PheIle 219
DB 868 CCTACTGGAGGTCTGGATCAGAGTCAACATCTGAAGACCCCAAGGTGACCTCTCGACT 927
QY 219 eAlaThrSerSerArgGlyThrGlyHisSerArgArgThrGlyLeu-----Al 235
DB 928 GTCTTCAGCAAGAGGGGGGAAAGGAAACAGTCACACGCCCTGTTTCGCTCTTGACGTC 987
QY 235 aCysArgThrSerLeu-----ProGlyLeuLysGluProAlaAlaSerLe 250
DB 988 ATGCAGACACAGCCCTGTCCTGAGGAGATGCCAGGGGCTCAAGGCCAAATGAC-CAGAC 1046
QY 250 uHisSerGluSerProArgGlyLysSerSerLeu----- 261
DB 1047 CTTGAGCCAGCCCAAAATGGATGAGCAGAGCTGAGTACTTCCCGCGGATCAGTGAGAC 1106
QY 262 -----LeuValSer-----LeuArgThrHisMetSerGlySe 272
DB 1107 ATCAGAGGACACAGACCTTTGGTGGATCGACAGTCTTCTCCCGGACACACAGACTCAGAC 1166
QY 272 rIleIle-----AlaPheLysValGlySerPheCysArgSerGluSerProVal-- 288
DB 1167 CAGCATAGAGCCAGGGCTGGGCAAGTCAAGCGAGAGAGAGGCTTAACAGTGGCGTGA 1226
QY 289 -----LeuHisGlnArgGluHisVal----- 295
DB 1227 CTACATCAAGATCACTCGAAGAGGCTCGGCTCACATTCACAGACAGATGTGTCCGGGTT 1286
QY 296 -GluLeuLeuArgGlyArgLysLeuAlaArgSerLeuAlaValLeuLeuSerAlaPheAl 315
DB 1287 GCACTTGAACCGAGAGCGGAAGGAGCAAGCAGTGTGGGTGTATCATGCGCAGCATTCAT 1346
QY 315 aIleCysThrPalaProTyrCysLeuPheThrIleValLeuSerThrTyrArgArg--G 334
DB 1347 TCTCTGCTGGATTCCTCTATTTTCATCTTCTATGTCATTCCTCTCTGTCGCAACAGCTGTG 1406
QY 334 yGluArgProLysSerIleTyrTyrSerIleAlaPheTyrLeuGlnTyrPheAsnSerLe 354
DB 1407 CAGCGAACCTGTG-----CACATGTTCACCATTTGGCTGGGCTACATCACTCCAC 1457
QY 354 uIleAsnProPheLeuTyrProLeuCysHisArgArgPheGlnLysAlaPheTyrPlysIl 374
DB 1458 GCTGAACCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1517
QY 374 eLeu 375
DB 1518 TCTG 1521

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RESULT 11

AK047070

LOCUS

DEFINITION

Mus musculus 10 days neonate cerebellum cDNA, RIKEN full-length  
enriched library, clone:B930016C09 product:HISTAMINE RECEPTOR HL,  
full insert sequence.

ACCESSION

AK047070

VERSION AK047070.1 GI:26338557

[illegible]

## FEATURES



Db 671 CACTTCAGCCCTCGCCCGCCAGAGCTTCGGGAAGATAGTGTGAGACAGATTCTTACAAT 730  
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Qy 200 ----- 200  
Db 851 ACCAAGCGGTCCCTCCCTACCTTTTATAGAAATCAAGCTGAGGTGCGGAGATGCCAAAGAG 910  
Qy 201 -----TTPSerLeuTyrLysArg----- 206  
Db 911 GGTGCCAAGAAACCTGGGAAGAGTCTCCCTGGGGGTCCAGAAGAGGCGGTCAAGAGAC 970  
Qy 207 -----GlySerLeuSerArgCysProSerHisAlaGly-PheI 219  
Db 971 CCTACTGGAGGTCTGGATCAGAAGTCAACATCTGAAGACCCCAAGGTGACCTCTCGACT 1030  
Qy 219 eAlaThrSerSerArgGlyThrGlyHisSerArgThrGlyLeu-----Al 235  
Db 1031 GTCTTCAGCCAAAGAGGGAAGGAAAGCAAGTCACAGCCCTCTGTTTTCGCTCTTGACGTC 1090  
Qy 235 aCysArgThrSerLeu-----ProGlyLeuLysGluProAlaAlaSerLe 250  
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Qy 250 uHisSerGluSerProArgGlyLysSerSerLeu----- 261  
Db 1150 CTTGAGCCAGCCAAATGGATGACAGAGCTGTAGTACTTCCGCGCGGATCAGTGAGAC 1209  
Qy 262 -----LeuValSer-----LeuArgThrHisMetSerGlyse 272  
Db 1210 ATCAGAGGACAGACCTTGGTGGATCGACAGTCTTCTCCCGGACCAAGACTCAGACAC 1269  
Qy 272 rIleIle-----AlaPheLysValGlySerPheCysArgSerGluSerProVal-- 288  
Db 1270 CAGCATAGAGCCAGGCTGGGCAAGTCAAGCCGAGAGACAGGTCTTAACAGTGGCCTGGA 1329  
Qy 289 -----LeuHisGlnArgGluHisVal----- 295  
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Qy 374 eLeu 375  
Db 1621 TCTG 1624

## RESULT 12

AK038480

LOCUS

DEFINITION Mus musculus adult male hypothalamus cDNA, RIKEN full-length enriched library, clone:A230019E03 product:HISTAMINE RECEPTOR H1, full insert sequence.

ACCESSION

AK038480

## VERSION

AK038480.1 GI:26332590

## KEYWORDS

HTC; CAP trapper.

## SOURCE

Mus musculus (house mouse)

## ORGANISM

Mus musculus

## REFERENCE

1 Carninci, P. and Hayashizaki, Y.

High-efficiency full-length cDNA cloning

Meth. Enzymol. 303, 19-44 (1999)

## AUTHORS

10349636

## TITLE

Normalisation and subtraction of cap-trapper-selected cDNAs to

prepare full-length cDNA libraries for rapid discovery of new genes

Genome Res. 10 (10), 1617-1630 (2000)

## JOURNAL

20499374

## MEDLINE

11042159

## PUBMED

20499374

## REFERENCE

2

Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,

Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M.,

Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,

Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,

Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,

Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,

Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.

RIKEN integrated sequence analysis (RISA) system--384-format

sequencing pipeline with 384 multicapillary sequencer

Genome Res. 10 (11), 1757-1771 (2000)

## JOURNAL

20530913

## MEDLINE

11076861

## PUBMED

11076861

## REFERENCE

4

The RIKEN Genome Exploration Research Group Phase II Team and the

FANTOM Consortium.

Functional annotation of a full-length mouse cDNA collection

Nature 409, 685-690 (2001)

## TITLE

The FANTOM Consortium and the RIKEN Genome Exploration Research

Group Phase I &amp; II Team.

Analysis of the mouse transcriptome based on functional annotation

of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

## JOURNAL

Nature 420, 563-573 (2002)

## REFERENCE

6 (bases 1 to 2379)

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,

Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, M.,

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Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,

Muramatsu, M. and Hayashizaki, Y.

Direct Submission

Submitted (16-JUN-2001) Yoshihide Hayashizaki, The Institute of

Physical and Chemical Research (RIKEN), Laboratory for Genome

Exploration Research Group, RIKEN Genomic Sciences Center (GSC),

RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,

Kanagawa 230-0045, Japan (E-mail: genome-res@gs.riken.jp,

URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,

Fax: 81-45-503-9216)

CDNA library was prepared and sequenced in Mouse Genome

Encyclopedia Project of Genome Exploration Research Group in Riken

Genomic Sciences Center and Genome Science Laboratory in RIKEN.

Division of Experimental Animal Research in Riken contributed to

prepare mouse tissues.

Please visit our web site for further details.

URL: http://genome.gsc.riken.jp/

URL: http://fantom.gsc.riken.jp/



## FEATURES

Location/Qualifiers  
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## CDS

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 Best Local Similarity: 26.14% Mismatches: 159  
 Query Match: 19.19% Indels: 118  
 DB: 3 Gaps: 18

## ORIGIN

US-10-626-126-9 (1-391) x AK038480 (1-2979)  
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 QY 21 LeuMetSerLeuLeuAlaPheAlaIleThrIleGly---AsnAlaValValIleLeuAla 39  
 DB 365 GTTCTAAGTAGTATCTCCCTG---GTACACAGTGGGCTCAACCTGCTGGTGTGTATGCA 421  
 QY 40 PheValAlaAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIle 59  
 DB 422 GTGCGCAGTGAGCGCAAGCTACACCGTGGGCACTGTGTACATTTGTACGCTGTCCGTA 481  
 QY 60 SerAspPhePheValGlyValIleSerIleProLeuTyrIleProHisThrLeuPhe--- 78  
 DB 482 GCAGACCTGATTGTAGGGGCGAGTCGTCATGCCCATCAACATCTCTATCTATCATGACC 541  
 QY 79 AsnTyrAsnProGlySerGlyIleCysMetPheTyrLeuIleThrAspTyrLeuLeuCys 98  
 DB 542 AAGTGTCTCTGGCGCGCCCTCTCCCTCTTTTGGCTCTCTATGATTATGTGGCCAGC 601  
 QY 99 ThrAlaSerValTyrSerIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsn 118  
 DB 602 ACGGCATCCATCTTTAGTGTCCTTCATCTGCTGTGATTGATCGCTACCGCTCTGTCCAGCA 661  
 QY 119 AlaValArgTyrArgAlaGlnHisThrGlyIleLeuLysIleValAlaGlnMetValAla 138  
 DB 662 CCCCTCGGTACCTGAGGTATCGAACCAAG---ACCCGTGCTTTCAGCTACCATCCTGGGG 718  
 QY 139 ValTyrIleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTyrLys 158  
 DB 719 GCCTGGTTCTCTCTCTCTGGGTATACCTATACTT-----GGCTGGCAT 766

QY 159 AsnSerThr-----AsnThrGluGluCysGluProGlyPheValThr 172  
 DB 767 CACTTCACGCCCTCGCCCCCAGAGCTTCGGGAAGATAAGTGTGAGACAGATTTCCTACAAT 826  
 QY 173 GluTyrTyrIleLeuAlaIleThrAlaPheLeuGluPheLeuLeuProValSerLeuVal 192  
 DB 827 GTCACTTGGTTCAGAGTATCATGCCCATCATCACTTCTACCTCCCACTTGGCTCATG 886  
 QY 193 ValTyrPheSerValGlnIleTyr----- 200  
 DB 887 CTGTGGTTCATGTATGAAGATCTACAAGGCTGTGCGCGACACTGTCTCAGCACCGCCAGCTC 946  
 QY 200 ----- 200  
 DB 947 ACCAACGGGTCCCTCCCTACCTCTTTTAAAGAACTCAAGTCTGAGGTCTGGAGGTGCAAGAG 1006  
 QY 201 -----TyrSerLeuTyrLysArg----- 206  
 DB 1007 GGTGCCCAAGAACTGGGAAAGAGTCTCCCTGGGGGTCCAGNAGAGGCGGTCAAGAGAC 1066  
 QY 207 -----GlySerLeuSerArgCysProSerHisAlaGly-Phe11 219  
 DB 1067 CCTACTGGAGGTCTGGATCAGAAGTCAACATCTGAAGACCCCAAGGTGACCTCTCCGACT 1126  
 QY 219 ealaThrSerSerArgGlyThrGlyHisSerArgThrGlyLeu-----Al 235  
 DB 1127 GTCTTCAGCAAGAGGGGAAAGGAAACAGTACACGCCCTCTTTCGCTCTTGACGTC 1186  
 QY 235 aCysArgThrSerLeu-----ProGlyLeuLysGluProAlaAlaSerLe 250  
 DB 1187 ATGCAGACACGCTGTGCTGAGGAGATGCCAGGGGTCAAGGCCAATGAC-CAGAC 1245  
 QY 250 uHisSerGluSerProArgGlyLysSerSerLeu----- 261  
 DB 1246 CTTGAGCCAGCCCAAAATGGATGAGCAGCAGCTGACTTTCGCCGGGATCAGTGAGAC 1305  
 QY 262 -----LeuValSer-----LeuArgThrHisMetSerGlySe 272  
 DB 1306 ATCAGAGCACCAGACCTTGTGTGATCGACAGTCTTCTCCCGGACCACAGACTCAGACAC 1365  
 QY 272 rIleIle-----AlaPheLysValGlySerPheCysArgSerGluSerProVal-- 288  
 DB 1366 CAGCATAGACCAGGGCTGGCAAGTCAAGCGAAGCAGAGTCTTAACAGTGGCTGGA 1425  
 QY 289 -----LeuHisGlnArgGluHisVal----- 295  
 DB 1426 CTACATCAAGTCACCTGGAAGAGGCTCCGCTCACATTCACAGACATGTGTGCCGGTT 1485  
 QY 296 -GluLeuLeuArgGlyArgLysLeuAlaArgSerLeuAlaValLeuLeuSerAlaPheAl 315  
 DB 1486 GCACCTTGAACCGAGAGCGGAAGCAGCAGCAGTGGGTGTGTATCATGCGACATTTCAT 1545  
 QY 315 aileCysTyrAlaProTyrCysLeuPheThrIleValLeuSerThrTyrArgArg---G1 334  
 DB 1546 TCTCTGCTGGATTCCTATTCATCTTCTTCATGGTCATGCTTCTGCAACAGCTGCTG 1605  
 QY 334 yGluArgProLysSerIleTyrSerIleAlaPheTyrLeuGlnTyrPheAsnSerLe 354  
 DB 1606 CAGCGAACCTGTG-----CACATGTCACCATTTGGCTGGGCTACATCACTCCAC 1656  
 QY 354 uIleAsnProPheLeuTyrProLeuCysHisArgArgPheGlnLysAlaPheTyrLysI1 374  
 DB 1657 GCTGAACCCCTCATCTACCGCTGTGCAACAGAACTTCAAGAAGACATTTCAAAAAAT 1716  
 QY 374 eLeu 375  
 DB 1717 TCTG 1720

## RESULT 13

AK046607 3783 bp mRNA linear HTC 03-APR-2004  
 Mus musculus 4 days neonate male adipose cDNA, RIKEN full-length  
 enriched library, clone:B430204G09 product:HISTAMINE RECEPTOR H1,  
 DEFINITION

ACCESSION	AK046607	full insert sequence.	URL: <a href="http://genome.gsc.riken.jp/">http://genome.gsc.riken.jp/</a>
VERSION	AK046607.1	GI:26338238	URL: <a href="http://fantom.gsc.riken.jp/">http://fantom.gsc.riken.jp/</a>
KEYWORDS	HTC; CAP trapper.		Location/Qualifiers
SOURCE	Mus musculus (house mouse)		1. 3783
ORGANISM	Mus musculus		/organism="Mus musculus"
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		/mol_type="mRNA"
AUTHORS	Carninci, P. and Hayashizaki, Y.		/strain="C57BL/6J"
TITLE	High-efficiency full-length cDNA cloning		/db_xref="PANTOM:DB:B430204G09"
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)		/db_xref="taxon:10090"
MEDLINE	99279253		/clone="B430204G09"
PUBMED	10349636		/sex="male"
REFERENCE	2		/tissue type="adipose"
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.		/clone_lib="RIKEN full-length enriched mouse cDNA library"
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes		/dev_stage="4 days neonate"
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)		247. 1713
MEDLINE	20499374		/note="unnamed protein product; HISTAMINE RECEPTOR H1 (SPR) [Q91V75, evidence: FASTY, 100%ID, 100%length, match=1464]"
PUBMED	11042159		putative"
REFERENCE	3		/codon_start=1
AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, S., Watahiki, M., Yoneda, Y., Iihiki, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.		/protein_id="BAC32805.1"
TITLE	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer		/db_xref="GI:26338239"
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)		/translation="MSLPNTSSASEDKMCEGNRTAMASPOLPLVVVLSISLVTVGL NLLVYAVRSRKLHTVGNLYSVLSVQADLVGVVMPNLYLIMTKWLSGRPLCLF WLSMDYVASTASIESVFLICIDRVSVQOPLRYLRTPKTRASATILGAWFLSFLMWI PILGWHHTPLAPLRDKCETDFVNTWFKIMTALINFLPTLLMLAFYKVKAVR RHQHRQLTNGSLPTFLIEIKLRSDEKAGKPKGKESPWGVQKPSRPTGGLDQKST SEDPKVTSPTVFSQEGRETVRCFLDVDMQTPVPEGDARGSKANDQTLISQPKQDE QSLSTRISSESDQTLVDQSPSRSTDSITSEPGLGKVKARSNSGLDIYKVTW KRLSHSRQVYSGLHNRKRAAKQLCIMAAFILCWPYIFPFMVIAPFCNSCCSEPV HMPTWLGVIINSTLNPLYIPLCNENFKKFKLHRS"
MEDLINE	20530913		
PUBMED	11076861		
REFERENCE	4		
AUTHORS	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.		
TITLE	Functional annotation of a full-length mouse cDNA collection		
JOURNAL	Nature 409, 695-690 (2001)		
MEDLINE	5		
PUBMED			
REFERENCE			
AUTHORS	The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.		
TITLE	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs		
JOURNAL	Nature 420, 563-573 (2002)		
MEDLINE	6 (bases 1 to 3783)		
PUBMED			
REFERENCE			
AUTHORS	Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.		
TITLE	Direct submission		
JOURNAL	Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration and Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gs.riken.jp, URL: <a href="http://genome.gsc.riken.jp/">http://genome.gsc.riken.jp/</a> , Tel: 81-45-503-9222, Fax: 81-45-503-9216)		
COMMENT	cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details.		

## ALIGNMENT SCORES:

Pred. No.:	6.9e-27	Length:	3783
Score:	392.50	Matches:	126
Percent Similarity:	42.74%	Conservative:	80
Best Local Similarity:	26.14%	Mismatches:	159
Query Match:	19.19%	Indels:	118
DB:	3	Gaps:	18

US-10-626-126-9 (1-391) x AK046607 (1-3783)

Qy	1	MetSerGluSerAsnGlyThrAspValLeuProLeuThrAlaGlnValProLeuAlaPhe	20
Db	286	ATGTGTAGGGGAACAGGACA---GCCATGGCAGCCCTCAGCTGCTGCCCTGGTGGTG	342
Qy	21	LeuMetSerLeuLeuAlaPheAlaIleThrIleGly---AsnAlaValValIleLeuAla	39
Db	343	GTTCCTAAGTAGTATCTCCCTG---GTCACAGTGGGGCCCTCAACCTGCTGGTGTATGCA	399
Qy	40	PheValAlaAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIle	59
Db	400	GTGCGCAGTAGCGGCAAGCTACACACCGTGGGCAACCTGTATGCTGACGCTCGGTA	459
Qy	60	SerAspPheValGlyValIleSerIleProLeuTyrIleProHisThrLeuPhe---	78
Db	460	GCAGACCTGATTAGGGGGGAGTGTGTATGCCATGAACATCTCTATCTATCATGACC	519
Qy	79	AsnTrpAsnProGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeuLeuCys	98
Db	520	AAGTGTCCCTGGGCGCCCTCTGCTCTTTGGCTCTCTATGATTATGTGGCCAGC	579
Qy	99	ThrAlaSerValTyrSerIleValleuleSerTyrAspArgTyrGlnSerValSerAsn	118
Db	580	ACGGCATCCATCTTTAGTGTCTTCACTCTGTATTGATCGCTACCGCTCTGTCCAGCA	639
Qy	119	AlaValArgTyrArgAlaGlnHisThrGlyIleLeuValIleValAlaGlnMetValAla	138
Db	640	CCCTCCCGTACTGAGGTATGGAACCAAG---ACCGTGTCTGACTACCACTCTGGGG	696
Qy	139	ValTrpIleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTrpIys	158

DEFINITION	Mus musculus HTR1B gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																		
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AUTHORS	Clark, A.G., Gnanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J., Adams, M.D. and Cargill, M.																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																		
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Score:	390.50																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																		
Percent Similarity:	46.81%																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																		
Best Local Similarity:	27.39%																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																		
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US-10-626-126-9 (1-391) x AY415607 (1-1161)																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																			
Qy	8	AspValLeuProLeuThrAlaGlnValProLeuAlaPheLeuMetSerLeuLeuAlaPhe	27																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																

RESULT 14  
AY415607  
LOCUS

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472 ACTCC---AAAGGGGGCCATCATGCTGCTGGTGTGGCTTCTCCATCTCTATT 528
Qy 147 AsnGlyProMetIleLeuAlaSerAspSerTrpIysAsnSerThrAsnThrGluGluCys 166
Db 529 TCGTGGCCACCTCTTTC-----TGGCGTCAAGCAAAAGCAGAGAGAGATG 576
Qy 167 GluProGlyPheValThrGluTrpIleLeu-----AlaIleThrAlaPheLeuGlu 184
Db 577 CTGACTGCTTTGTGAACACCGACGCTCTCTACACGGTCTACTCCACGGTGGCGCT 636
Qy 185 PheLeuLeuProValSerLeuValValTrpPheSerValGlnIleTrpSerLeuTrp 204
Db 637 TTTATTTACCCACCTCTCTCATCGCCCTCTATGCGCCGCACTATGTGAAGCCCGC 696
Qy 205 LysArgGlySerLeuSerArgCysProSerHisAlaGlyPheIleAlaThrSerSerArg 224
Db 697 TCTCGG---ATTTTGAACACAGACCCCAACAAAGACCGC----- 732
Qy 225 GlyThrGlyHisSerArgArgThrGlyLeuAlaCysArgThrSerLeuProGlyLeuLys 244
Db 733 -----AAGCGGTTGACCGCGACCGCAGTTGATAACAGACTCCCGGGATCCACA 780
Qy 245 GluProAlaAlaSerLeuHisSerGluSerProArgGlyLysSerSerLeuLeuValSer 264
Db 781 TCCTCGGTCACTCCATTAACTCCCGGCTCCGGAGTGGCCAGTGAG----- 828
Qy 265 LeuArgThrHisMetSerGlySerIleIleAlaPheLysValGlySerPheCysArgSer 284
Db 829 -----TCCGGGTCTCTCTGTG-----TACGTGAACCAAGTCAAAAGTGCGA 867
Qy 285 GluSerProValLeuHisGlnArgGluHisValGluLeuLeuArgGlyArgGlyLeuAla 304
Db 868 GTCTCAGAGCCCTGCTCGAAAGAAAGAACTCATGCGCGCTAGGAGCGCAAGCCACC 927
Qy 305 ArgSerLeuAlaValLeuLeuSerAlaPheAlaIleCysTrpAlaProTyrCysLeuPhe 324
Db 928 AAGACCTTAGGATCATTTAGGAGCAITTTATGTGTGTGGTGGCTCTTCTCATCATC 987
Qy 325 ThrIleValLeuSerThrTyrArgArgGlyGluArgProLysSerIleTrpTyrSerIle 344
Db 988 TCCCTGGTGTATCGCTATCTGTAAG-----GATCGTGTGGTTTCACATG 1032
Qy 345 AlaPhe-----TrpLeuGlnTrpPheAsnSerLeuIleAsnProPheLeu 359
Db 1033 GCCATTTTGTACTTCTCAATGTGTAGGCTATCTTAATCTCCTCATCAACCCATCATC 1092
Qy 360 TyrProLeuCysHisArgArgPheGlnLysAlaPheTrpLysIleLeu 375
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RESULT 15
AY415605
LOCUS
DEFINITION
Homo sapiens HTR1B gene, VIRTUAL TRANSCRIPT, partial sequence,
Genomic survey sequence.
ACCESSION
AY415605
VERSION
AY415605.1 GI:39771564
KEYWORDS
GSS.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1173)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civeello, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
source
1..1173
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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/gene="HTR1B"
/locus_tag="HMS5613"

ORIGIN
Alignment Scores: 3.2e-27 Length: 1173
Pred. No.: 387.50 Matches: 105
Score: 46.42% Conservative: 70
Percent Similarity: 27.85% Mismatches: 159
Best Local Similarity: 18.95% Indels: 43
Query Match: 9 Gaps: 11
DB: 11

US-10-626-126-9 (1-391) x AY415605 (1-1173)
Qy 8 AspValLeuProLeuThrAlaGlnValProLeuAlaPheLeuMetSerLeuLeuAlaPhe 27
Db 124 GACTCCATCCCTACCTGGAAAGTACTGCTGTTATGCTATTGGCGCTCATCACCTTG 183
Qy 28 AlaIleThrIleGlyAsnAlaValValIleLeuAlaPheValAlaAspArgAsnLeuArg 47
Db 184 GCCACCAAGCTCTCCAAATGCTTTGTGATGCCAGTGTACCGGACCCGGAACACTGCAC 243
Qy 48 HisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSerAspPhePheValGlyValIle 67
Db 244 ACCCGGGTAACTACTGATGCTGCTCTGCGGTGTCACCGACCTGCTGTGTGCTCCATCTG 303
Qy 68 SerIleProLeuTyrIleProHisThrLeuPhe---AsnTrpAsnProGlySerGlyIle 86
Db 304 GTGATGCCATCAGCACCACTGATACACTGTCACCGCGCTGACACATGGCCAGGTGTC 363
Qy 87 CysMetPheTrpLeuIleThrAspTyrLeuLeuCysThrAlaSerValTyrSerIleVal 106
Db 364 TGTGACTTCTGGCTGTCTCGGACATCATCTTGTGTCATGCTCCATCTCCATCTGT 423
Qy 107 LeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaValArgTyrArgAlaGlnHis 126
Db 424 GTCATCGCCCTGGACCGCTACTGGGCATACAGGACGCGGTGGAGTACTCAGCTAAAGG 483
Qy 127 ThrGlyIleLeuLysIleValAlaGlnMetValAla---ValTrpIleLeuAlaPheLeu 145
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Qy 146 ValAsnGlyProMetIleLeuAlaSerAspSerTrpLysAsnSerThrAsnThrGluGlu 165
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Qy 166 CysGluProGlyPheValThrGluTrpTyrIleLeu-----AlaIleThrAlaPheLeu 183
Db 586 GTGTGGGAATCGGTGGTGAACACCGACCACTCTCTACAGGTCTACTCCACGGTGGGT 645
Qy 184 GluPheLeuLeuProValSerLeuValValTrpPheSerValGlnIleTyrTrpSerLeu 203
Db 646 GCTTTTACTTCCCAACCCCTCTCTCATCGCCCTCTATGCGCGCATCTACGTAGAAGCC 705
Qy 204 TrpLysArgGlySerLeuSerArgCysProSerHisAlaGlyPheIleAlaThrSerSer 223
Db 706 CGTCCCGG---ATTTTGAACACAGACCGCCCAACAGGACCGGC----- 744
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Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,  
Todd, M.A., Tanenbaum, D.M., Civeello, D.R., Lu, F., Murphy, B.,  
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,  
Adams, M.D. and Cargill, M.  
Direct Submission  
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
Rockville, MD 20850, USA  
This sequence was made by sequencing genomic exons and ordering  
them based on alignment.

FEATURES  
source  
1..1173  
Location/Qualifiers

gene  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"

<1..>1173  
/gene="HTR1B"  
/locus\_tag="HMS5613"

Alignment Scores: 3.2e-27 Length: 1173  
Pred. No.: 387.50 Matches: 105  
Score: 46.42% Conservative: 70  
Percent Similarity: 27.85% Mismatches: 159  
Best Local Similarity: 18.95% Indels: 43  
Query Match: 9 Gaps: 11  
DB: 11

US-10-626-126-9 (1-391) x AY415605 (1-1173)

Qy 8 AspValLeuProLeuThrAlaGlnValProLeuAlaPheLeuMetSerLeuLeuAlaPhe 27  
Db 124 GACTCCATCCCTACCTGGAAAGTACTGCTGTTATGCTATTGGCGCTCATCACCTTG 183  
Qy 28 AlaIleThrIleGlyAsnAlaValValIleLeuAlaPheValAlaAspArgAsnLeuArg 47  
Db 184 GCCACCAAGCTCTCCAAATGCTTTGTGATGCCAGTGTACCGGACCCGGAACACTGCAC 243  
Qy 48 HisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSerAspPhePheValGlyValIle 67  
Db 244 ACCCGGGTAACTACTGATGCTGCTCTGCGGTGTCACCGACCTGCTGTGTGCTCCATCTG 303  
Qy 68 SerIleProLeuTyrIleProHisThrLeuPhe---AsnTrpAsnProGlySerGlyIle 86  
Db 304 GTGATGCCATCAGCACCACTGATACACTGTCACCGCGCTGACACATGGCCAGGTGTC 363  
Qy 87 CysMetPheTrpLeuIleThrAspTyrLeuLeuCysThrAlaSerValTyrSerIleVal 106  
Db 364 TGTGACTTCTGGCTGTCTCGGACATCATCTTGTGTCATGCTCCATCTCCATCTGT 423  
Qy 107 LeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaValArgTyrArgAlaGlnHis 126  
Db 424 GTCATCGCCCTGGACCGCTACTGGGCATACAGGACGCGGTGGAGTACTCAGCTAAAGG 483  
Qy 127 ThrGlyIleLeuLysIleValAlaGlnMetValAla---ValTrpIleLeuAlaPheLeu 145  
Db 484 ACTCC-----AAGAGGGCGCGGTGATGATCGCGTGGTGGTGGTCTTCTCCATCTCT 537  
Qy 146 ValAsnGlyProMetIleLeuAlaSerAspSerTrpLysAsnSerThrAsnThrGluGlu 165  
Db 538 ATCTCGTGTGCGCGCTTCTTC-----TGGCGTCAAGCTAAGCCGCAAGAGGAG 585  
Qy 166 CysGluProGlyPheValThrGluTrpTyrIleLeu-----AlaIleThrAlaPheLeu 183  
Db 586 GTGTGGGAATCGGTGGTGAACACCGACCACTCTCTACAGGTCTACTCCACGGTGGGT 645  
Qy 184 GluPheLeuLeuProValSerLeuValValTrpPheSerValGlnIleTyrTrpSerLeu 203  
Db 646 GCTTTTACTTCCCAACCCCTCTCTCATCGCCCTCTATGCGCGCATCTACGTAGAAGCC 705  
Qy 204 TrpLysArgGlySerLeuSerArgCysProSerHisAlaGlyPheIleAlaThrSerSer 223  
Db 706 CGTCCCGG---ATTTTGAACACAGACCGCCCAACAGGACCGGC----- 744

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QY 224 ArgGlyThrGlyHisSerArgArgThrGlyLeuAlaCysArgThrSerLeuProGlyLeu 243
Db -----AAGCGCTTGAGCCGAGCCAGCTGATAACCGACTCCCGGGTCC 789
QY 244 LysGluProAlaAlaSerLeuHisSerGluSerProArgGlyLysSerSerLeuVal 263
Db -----TCCGGATCTCCTGTG-----TATGTGAACCAAGTCAAAAGTG 840
QY 264 SerLeuArgThrHisMetSerGlySerIleIleAlaPheLysValGlySerPheCysArg 283
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QY 284 SerGluSerProValLeuHisGlnArgGluHisValGluLeuLeuArgGlyArgLysLeu 303
Db CGAGTCTCCGAGCCCTGCTGGAAAGAGAAACTCATGGCCGCTAGGGAGCGCAAGCC 936
QY 304 AlaArgSerLeuAlaValLeuLeuSerAlaPheAlaIleCysTrpAlaProTyrCysLeu 323
Db ACCAGACCTAGGGATCATTTGGGAGCCTTATTGTGTGTGGCTACCTTCTTCATC 996
QY 324 PheThrIleValLeuSerThrTyrArgArgGlyGluArgProLysSerIleTrpTyrSer 343
Db ATCTCCCTAGTGATGCTATCTGAAA-----GATGCTGCTGTTCCAC 1041
QY 344 IleAlaPhe-----TrpLeuGlnTrpPheAsnSerLeuIleAsnProphe 358
Db CTAGCCATCTTTGACTTCTTCACATGGCTGGGCTATCTCAACTCCCTCATCAACCCATA 1101
QY 359 LeuTyrProLeuCysHisArgArgPheGlnLysAlaPheTrpLysIleLeu 375
Db ATCTATACCATGTCCCAATGAGGACTTTAAACAGCATTCATTAATACTGATA 1152
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Search completed: August 5, 2005, 17:26:09  
Job time : 3195 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 3, 2005, 01:37:47 ; Search time 170 Seconds  
(without alignments)  
1177.782 Million cell updates/sec

Title: US-10-626-126-9  
Perfect score: 2045  
Sequence: 1 MSESNGTDVLPFTAQVPLAF.....WKILCTKQAPASQTSVSS 391

Scoring table:  
BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Uniprot 03: \*  
1: uniprot\_sprot: \*  
2: uniprot\_trembl: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2034	99.5	391	2 Q912Y1	Q912y1 rattus norv
2	1742	85.2	391	2 Q912Y2	Q912y2 mus musculu
3	1405.5	68.7	390	2 Q961D9	Q961d9 homo sapien
4	1403.5	68.6	390	1 HH4R HUMAN	Q9h3n8 homo sapien
5	1328.5	65.0	390	2 Q8WVJ9	Q8wnv9 sus scrofa
6	1237.5	60.5	389	2 Q912Y3	Q912y3 cavia porce
7	698	34.1	445	2 Q865E1	Q865e1 macaca mula
8	697.5	34.1	445	1 HH3R CAVPO	Q9j135 cavia porce
9	693	33.9	445	1 HH3R HUMAN	Q9y5n1 homo sapien
10	686	33.5	445	1 HH3R MOUSE	P58406 mus musculu
11	682	33.3	445	1 HH3R RAT	Q9qyn8 rattus norv
12	671	32.8	473	2 Q6ZM33	Q6zm33 brachydanio
13	658	32.2	365	2 Q8WY01	Q8wy01 homo sapien
14	658	32.2	373	2 Q8WX29	Q8wx29 homo sapien
15	577	28.2	175	2 Q6J9J5	Q6j9j5 pan troglod
16	572	28.0	174	2 Q6J9J4	Q6j9j4 gorilla gor
17	466.5	22.8	301	2 Q8WY00	Q8wy00 homo sapien
18	466.5	22.8	309	2 Q8N149	Q8n149 homo sapien
19	410.5	20.1	590	1 ACM3 BOVIN	P41984 bos taurus
20	408.5	20.0	590	1 ACM3 FIG	P11483 sus scrofa
21	403.5	19.7	590	1 ACM3 GORGO	Q9n2a3 gorilla gor
22	403.5	19.7	590	1 ACM3 HUMAN	P20309 homo sapien
23	403.5	19.7	590	1 ACM3 PANTR	Q9n2a4 pan troglod
24	402.5	19.7	590	1 ACM3_PONPY	Q9n2a2 pongo pygma
25	401.5	19.6	491	1 HH1R BOVIN	P30546 bos taurus
26	401.5	19.6	530	2 Q8VH24	Q8vh24 cavia porce
27	401	19.6	531	1 ACM5 RAT	P08911 rattus norv
28	400.5	19.6	410	2 Q86GT6	Q86gt6 caenorhabdi
29	400.5	19.6	422	2 Q8T3C1	Q8t3c1 caenorhabdi
30	400.5	19.6	435	2 Q22895	Q22895 caenorhabdi
31	400	19.6	532	1 ACM5_HUMAN	P08912 homo sapien

ALIGNMENTS

RESULT 1

ID	Q912Y1	PRELIMINARY;	PRT;	391 AA.
AC	Q912Y1;			
DT	01-DEC-2001 (TrEMBLrel. 19, Created)			
DT	01-DEC-2001 (TrEMBLrel. 19, Last sequence update)			
DT	01-JUN-2003 (TrEMBLrel. 24, Last annotation update)			
DE	Histamine H4 receptor.			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
OX	NCBI_TaxID=10116;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=Sprague-Dawley;			
RA	Liu C., Wilson S., Kuei C., Lovenberg T.W.;			
RL	Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.			
CC	- - SURCELLULAR LOCATION: Integral membrane protein (By similarity).			
CC	- - SIMILARITY: Belongs to family 1 of G-protein coupled receptors.			
DR	EMBL; AF358860; AAK97381.1; -			
DR	GO; GO:0016021; C:integral to membrane; IEA.			
DR	GO; GO:0004872; F:receptor activity; IEA.			
DR	GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.			
DR	GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.			
DR	Pfam; PF00001; 7tm 1; 1.			
DR	PRINTS; PR00237; GPCRHHODOPSN.			
DR	PRINTS; PR01726; HISTAMINEH4R.			
DR	PROSITE; PS00237; G PROTEIN RECP F1.1; 1.			
DR	PROSITE; PS02622; G_PROTEIN_RECEP_F1_2; 1.			
KW	G-protein coupled receptor; Receptor; Transmembrane.			
SQ	SEQUENCE 391 AA; 44023 MW; C707BA6E39CFD41 CRC64;			

Query Match 99.5%; Score 2034; DB 2; Length 391;  
Best Local Similarity 99.7%; Pred. No. 4.4e-142;  
Matches 390; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db	121	RYRAQHTGILKIVQAVVAVILAFVNGPMLASDSWKSNSTNTECEPGFVTEWYILAIT 180		
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Db	181	AFLEFLLPVLVYVFSQIYWSLWKRGSLSRCSHAGFIATSRGTGHSRRTGLACRTSL 240		
Qy	241	PGKPEAASHSESPKGSLLVSLTHMSGSLIAFKVGSFCSESPVLHOREHVELLRC 300		



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Db 241 PGLKEPAASLHSES PRGKSSLLVSLRTHMSGI IAFKVGSCRSBPVLHQREHVLLRG 300
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Db 301 RKLARSLAVLSAFAICWAPYCLFTIVLSTYRGRPKSIWYSIAFWLQWPNLSINPFLY 360
Qy 361 PLCHRRFOKAFWKILCVTKQAPSPQTSQSVSS 391
Db 361 PLCHRRFOKAFWKILCVTKQAPSPQTSQSVSS 391

RESULT 2
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AC Q91ZY2;
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DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Histamine H4 receptor.
GN Name=H4h4;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RA Liu C., Wilson S., Kuei C., Lovenberg T.W.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
DR EMBL; AF358859; AAK97380.1; -.
DR MGD; MGI:2429635; Hrh4.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0005887; C:integral to plasma membrane; IC.
DR GO; GO:0005624; C:membrane fraction; IDA.
DR GO; GO:0004969; F:histamine receptor activity; IDA.
DR GO; GO:0006954; P:inflammatory response; TAS.
DR Pfam; PF00001; 7cm1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PR01726; HISTAMINEH4R.
DR PROSITE; PS00237; G-PROTEIN RECEPTOR_F1_1; 1.
DR PROSITE; PS00262; G-PROTEIN RECEPTOR_F1_2; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 391 AA; 44248 MW; 59EC73CB5214C5E0 CRC64;

Query Match 85.2%; Score 1742; DB 2; Length 391;
Best Local Similarity 84.9%; Pred. No. 1.6e-120;
Matches 332; Conservative 17; Mismatches 42; Indels 0; Gaps 0;

Qy 1 MSESNGTDVLPATAQVPLAFLMSLLAFATIGNAVVILAFVADRNLHRHSNYFFLNLAIS 60
Db 1 MSESNGTILPPAAQVPLAFLMSFAFAIMVGNVAVILAFVVDRLHRHSNYFFLNLAIS 60
Qy 61 DPFVGVISIPLYIPHTLFNNWPGSGICMFWLITDYLLCTASVYVLSIDRYQSVSNV 120
Db 61 DFLVGLISIPLYIPHTLFNNWPGSGICMFWLITDYLLCTASVYVLSIDRYQSVSNV 120
Qy 121 RYRAQHTGILKIVAQMVAVIILAFVNGPMLASDSWKNSTNTERCEPGFVTEWILAIT 180
Db 121 SYRAQHTGIMKIVAQMVAVIILAFVNGPMLASDSWKNSTNTERCEPGFVTEWILAIT 180
Qy 181 AFLEPFLPVLSVYVSVQIYNSLWKGSLRSCPSHAGFIATSSRGTHSRRTGLACRTSL 240
Db 181 SYRAQHTGIMKIVAQMVAVIILAFVNGPMLASDSWKNSTNTERCEPGFVTEWILAIT 180
Qy 241 PGLKEPAASLHSES PRGKSSLLVSLRTHMSGI IAFKVGSCRSBPVLHQREHVLLRG 300
Db 241 PGLKEPAASLHSES PRGKSSLLVSLRTHMSGI IAFKVGSCRSBPVLHQREHVLLRG 300
Qy 301 RKLARSLAVLSAFAICWAPYCLFTIVLSTYRGRPKSIWYSIAFWLQWPNLSINPFLY 360
Db 301 RKLARSLAVLSAFAICWAPYCLFTIVLSTYRGRPKSIWYSIAFWLQWPNLSINPFLY 360
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Qy 361 PLCHRRFOKAFWKILCVTKQAPSPQTSQSVSS 391
Db 361 PLCHRRFOKAFWKILCVTKQAPSPQTSQSVSS 391

RESULT 3
Q96LD9 PRELIMINARY; PRT; 390 AA.
AC Q96LD9;
DT 01-DEC-2001 (TREMELrel. 19, Created)
DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)
DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)
DE Histamine receptor H4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21106319; PubMed=11179435;
RA Nguyen T., Shapiro D.A., George S.R., Setola V., Lee D.K., Cheng R.,
RA Rauser L., Lee S.P., Lynch K.R., Roth B.L., O'Dowd B.F.;
RT "Discovery of a novel member of the histamine receptor family. ";
RL Mol. Pharmacol. 59:427-433(2001)
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
DR EMBL; AY008280; AAL09297.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; F:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR00276; GPCR Rhodpsn.
DR InterPro; IPR008102; Histaminrecept_H4.
DR Pfam; PF00001; 7cm1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PRINTS; PR01726; HISTAMINEH4R.
DR PROSITE; PS00237; G-PROTEIN RECEPTOR_F1_1; 1.
DR PROSITE; PS00262; G-PROTEIN RECEPTOR_F1_2; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 390 AA; 44469 MW; CC82B5D30D216C66 CRC64;

Query Match 68.7%; Score 1405.5; DB 2; Length 390;
Best Local Similarity 69.1%; Pred. No. 1e-95;
Matches 271; Conservative 41; Mismatches 77; Indels 3; Gaps 2;

Qy 1 MSESNGTDVLPATAQVPLAFLMSLLAFATIGNAVVILAFVADRNLHRHSNYFFLNLAIS 60
Db 1 MADTNTINLSLSTRVTLAFPMSLVAFALMGLNALVILAFVVDKLRHRSNYFFLNLAIS 60
Qy 61 DPFVGVISIPLYIPHTLFNNWPGSGICMFWLITDYLLCTASVYVLSIDRYQSVSNV 120
Db 61 DPFVGVISIPLYIPHTLFNNWPGSGICMFWLITDYLLCTASVYVLSIDRYQSVSNV 120
Qy 121 RYRAQHTGILKIVAQMVAVIILAFVNGPMLASDSWKNSTNTERCEPGFVTEWILAIT 180
Db 121 SYRTQHTGVLKIVAVVILAFVNGPMLIVSVESWKEGS--ECEPGFPFSEWILAIT 178
Qy 181 AFLEPFLPVLSVYVSVQIYNSLWKGSLRSCPSHAGFIATSSRGTHSRRTGLACRTSL 240
Db 179 SFLEFVIFVILVAYFNMMIYNSLWKRDLHSLRCSQHPGLTAVSSNICGHSFRGLSSRRSL 238
Qy 241 PGLKEPAASLHSES PRGKSSLLVSLRTHMSGI IAFKVGSCRSBPVLHQREHVLLRG 300
Db 239 SASTVEPASFSESRQRKSSLMFSSRTNNSNTIASKMGSPSQSDSVALHQREHVLLRA 298
Qy 301 RKLARSLAVLSAFAICWAPYCLFTIVLSTYRGRPKSIWYSIAFWLQWPNLSINPFLY 360
Db 299 RLAKSLAILLGVFVAVCAPVSLFTIVLSFTSSATGPKSVWTRIAFWLQWPNLSINPFLY 358
Qy 361 PLCHRRFOKAFWKILCVTKQAPSPQTSQSVSS 391
Db 359 PLCHRRFOKAFWKILCVTKQAPSPQTSQSVSS 390
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RESULT 4  
HH4R HUMAN STANDARD; PRT; 390 AA.  
AC Q9H3N8; Q9CZQ0;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 25-OCT-2004 (Rel. 45, Last annotation update)  
DE Histamine H4 receptor (HH4R) (GPRV53) (G protein-coupled receptor 105)  
DE (GPCR105) (SP9144) (AXOR35).  
GN Name=HH4;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20538417; PubMed=10973974; DOI=10.1074/jbc.M006480200;  
RA Oda T., Morikawa N., Saito Y., Masuho Y., Matsumoto S.-I.;  
RT "Molecular cloning and characterization of a novel type of histamine  
RT receptor preferentially expressed in leukocytes.";  
RL J. Biol. Chem. 275:36781-36786(2000).  
RN [2]  
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.  
RC TISSUE=Leukocyte;  
RX MEDLINE=20568725; PubMed=11118334; DOI=10.1006/bbrc.2000.4008;  
RA Nakamura T., Itadani H., Hidaka Y., Ohta M., Tanaka K.;  
RT "Molecular cloning and characterization of a new human histamine  
RT receptor, HH4R.";  
RL Biochem. Biophys. Res. Commun. 279:615-620(2000).  
RN [3]  
RP SEQUENCE FROM N.A.  
RA Jones P.G., Wu S., Betty M.;  
RT "Cloning of a novel histamine receptor.";  
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.  
RC TISSUE=Bone marrow;  
RX PubMed=11179434;  
RA Liu C., Ma X.-J., Jiang X., Wilson S.J., Hofstra C.L., Blevitt J.,  
RA Pyati J., Li X., Chai W., Carruthers N., Lovenberg T.W.;  
RT "Cloning and pharmacological characterization of a fourth histamine  
RT receptor (H4) expressed in bone marrow.";  
RL Mol. Pharmacol. 59:420-426(2001).  
RN [5]  
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.  
RC TISSUE=Eosinophil;  
RX MEDLINE=21104636; PubMed=11181941;  
RA Morse K.L., Behan J., Laz T.M., West R.E. Jr., Greenfeder S.A.,  
RA Anthes J.C., Umland S., Wan Y., Hipkin R.W., Gonsiorek W., Shin N.,  
RA Gustafson E.L., Qiao X., Wang S., Hedrick J.A., Greene J., Bayne M.,  
RA Monstafa F.J. Jr.;  
RT "Cloning and characterization of a novel human histamine receptor.";  
RL J. Pharmacol. Exp. Ther. 296:1058-1066(2001).  
RN [6]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21106320; PubMed=11179436;  
RA Zhu Y., Michalovich D., Wu H.-L., Tan K.B., Dytko G.M., Mannan I.J.,  
RA Boyce R., Alston J., Tierney L.A., Li X., Herrity N.C., Vawter L.,  
RA Sarau H.M., Ames R.S., Davenport C.M., Hieble P., Wilson S.,  
RA Bergema D.J., Fitzgerald L.R.;  
RT "Cloning, expression, and pharmacological characterization of a novel  
RT human histamine receptor.";  
RL Mol. Pharmacol. 59:434-441(2001).  
RN [7]  
RP SEQUENCE FROM N.A.  
RA O'Reilly M.A.;  
RT "Identification of a histamine H4 receptor on human eosinophils - Role  
RT in eosinophil chemotaxis.";  
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.  
RN [8]  
RP SEQUENCE FROM N.A.

RA Puhl H.L. III, Ikeda S.R., Aronstam R.S.;  
RT "cDNA clones of human proteins involved in signal transduction  
RT sequenced by the Guthrie cDNA resource center (www.cdna.org).";  
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: The H4 subclass of histamine receptors could mediate the  
CC histamine signals in peripheral tissues. Displays a significant  
CC level of constitutive activity (spontaneous activity in the  
CC absence of agonist).  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -!- TISSUE SPECIFICITY: Expressed primarily in the bone marrow and  
CC eosinophils. Shows preferential distribution in cells of  
CC immunological relevance such as T-cells, dendritic cells,  
CC monocytes, mast cells, neutrophils. Also expressed in a wide  
CC variety of peripheral tissues, including the heart, kidney, liver,  
CC lung, pancreas, skeletal muscle, prostate, small intestine,  
CC spleen, fetal liver and lymph node.  
CC -!- INDUCTION: Expression is either up-regulated or down-regulated  
CC upon activation of the lymphoid tissues and this regulation may  
CC depend on the presence of IL-10 or IL-13.  
CC -!- MISCELLANEOUS: Does not bind diphenhydramine, loratadine,  
CC ranitidine, cimetidine and chlorpheniramine. Shows modest affinity  
CC for dimaprit, imipromidine, clobenpropit, thioperamide, burimamide  
CC clobapine, imipip and imetit. The order of inhibitory activity  
CC was imetit > clobenpropit > burimamide > thioperamide.  
CC Clobenpropit behaves as a partial agonist, dimaprit and  
CC imipromidine show some agonist activity while clobapine behaves as  
CC a full agonist. Thioperamide shows inverse agonism (enhances CAMP  
CC activity). The order of inhibitory activity of histamine  
CC derivatives was Histamine > N-alpha-methylhistamine > R(-)-alpha-  
CC methylhistamine > S(+)-alpha-methylhistamine. Both N-alpha-  
CC methylhistamine > R(-)-alpha-methylhistamine behave as full  
CC agonists.  
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.  
CC  
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CC or send an email to license@isb-sib.ch).  
CC  
CC EMBL; AB044934; BAB13698.1; -  
CC EMBL; AB045370; BAB20091.1; -  
CC EMBL; AF307973; AAG32052.1; -  
CC EMBL; AF312230; AAK12081.1; -  
CC EMBL; AF329449; AAK43542.1; -  
CC EMBL; AF325356; AAL01684.1; -  
CC EMBL; AF298292; CAC83493.1; -  
CC EMBL; AY136745; AAN01271.1; -  
CC PIR; JC7566; JC7566.  
CC Genew; HGNC:17383; HRR4.  
CC MIM; 606792; -  
CC CO; GO:0016021; C:integral to membrane; NAS.  
CC GO; GO:0004969; F:histamine receptor activity; NAS.  
CC InterPro; IPR000276; GPCR\_Rhodops.  
CC InterPro; IPR008102; Histamrecept\_H4.  
CC Pfam; PF00001; 7tm 1; 1.  
CC PRINTS; PR00237; GPCRHHODOPS.  
CC PRINTS; PR01726; HISTAMINEH4R.  
CC PROSITE; PS00337; G-PROTEIN RECEPTOR FL1; 1.  
CC PROSITE; PS03262; G-PROTEIN RECEPTOR FL2; 1.  
CC G-protein coupled receptor; Glycoprotein; Lipoprotein; Palmitate;  
CC Transmembrane.  
CC DOMAIN 1 19 Extracellular (Potential).  
CC TRANSMEM 20 40 1 (Potential).  
CC DOMAIN 41 52 Cytoplasmic (Potential).  
CC TRANSMEM 53 73 2 (Potential).  
CC DOMAIN 74 87 Extracellular (Potential).  
CC TRANSMEM 88 108 3 (Potential).  
CC DOMAIN 109 131 Cytoplasmic (Potential).  
CC TRANSMEM 132 152 4 (Potential).  
CC DOMAIN 153 172 Extracellular (Potential).

TRANSMEM 173 5 (Potential).  
FT DOMAIN 194 Cytoplasmic (Potential).  
FT TRANSMEM 304 6 (Potential).  
FT DOMAIN 325 Extracellular (Potential).  
FT TRANSMEM 341 7 (Potential).  
FT DOMAIN 342 7 (Potential).  
FT TRANSMEM 363 Cytoplasmic (Potential).  
FT DISULFID 87 By similarity.  
FT CARBOHYD 5 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 9 N-linked (GlcNAc...) (Potential).  
FT LIPID 374 S-palmitoyl cysteine (Potential).  
FT CONFLICT 138 A -> V (in Ref. 1).  
FT CONFLICT 206 H -> R (in Ref. 1).  
FT CONFLICT 253 Q -> R (in Ref. 1).  
SQ SEQUENCE 390 AA; 44495 MW; C986B8AE7FF912C3 CRC64;

Query Match 68.6%; Score 1403.5; DB 1; Length 390;  
Best Local Similarity 69.1%; Pred. No. 1.5e-95;  
Matches 271; Conservative 40; Mismatches 78; Indels 3; Gaps 2;

QY 1 MSESNGTVLPLTAQVPLAFVLAFAITIGNAVVILAFVADNLRHRSNYFFLNLAIS 60  
Db 1 MPDTNSTINLSUSTRVTLAFPSLVAFAPMLGNALVILAFVVDKLRHRSYFFLNLAIS 60  
QY 61 DFFVGVISIPYIPHTLFNNWPGSGICMFWLTIDYLLCTASVYSIVLISYDRYQSVNAV 120  
Db 61 DFFVGVISIPYIPHTLFEMDPGKEICVFWLTIDYLLCTASVYNIVLISYDRYLSVNAV 120  
QY 121 RYRAQHTGILKIVAOQVAVVILAFVNGPMILASDWKNSNTWTECEPGVTEWYILAIT 180  
Db 121 SYRTQHTGILKIVAVVILAFVNGPMILVSESKDEG3--BCEPGFFSEWYILAIT 178  
QY 181 APLFELLVSVLVVFSVOIYVSLWKGSI.SRCPSHAGFIATSRGTGHSRRRTGLACRTSL 240  
Db 179 SFLEFVIVPVLVAYFNNMIYVSLWKRDLHLSRCQSHPLGTAVSSNICGHSFGRLSRRSL 238  
QY 241 POLKEPAASLHSES PRGKSSLLVSLRTHMSGIIAFKVGSCFRCSPVILHOREHVELLRG 300  
Db 239 SASTVPASFHSERQRRKSSLMFSSRTKWNSTIASKMGSPSQSDSVALHOREHVELLRA 298  
QY 301 RKLARSLAVLSAFAICWAPYCLFTIVLSTYRGRPKSIWYSIAFWLQFNLSINPLFY 360  
Db 299 RLAKSLAILLGVPVAVCAPYSLFTIVLSFYSSATGPKSVVYRIAFWLMQFNFSVYNPLLY 358  
QY 361 PLCHRRFOKAFWKILCVTKQAPSPQ-TOSVSS 391  
Db 359 PLCHRRFOKAFWKILCVTKQAPSPQSHRSVSS 390

RESULT 5  
Q8MNV9 PRELIMINARY; PRT; 390 AA.  
ID Q8MNV9  
AC Q8MNV9  
DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Histamine H4 receptor.  
OS Sus scrofa (Pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.  
OX NCBI\_TaxID=9823;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Spleen.  
RX MEDLINE=22015261; PubMed=12020829; DOI=10.1016/S0167-4781(02)00236-1;  
RA Oda T., Matsumoto S., Masuho Y., Takasaki J., Matsumoto M.,  
RA Kamohara M., Saito T., Onishi T., Soga T., Hiyama H., Matsushima H.,  
RA Furuichi K.;  
RT "cDNA cloning and characterization of porcine histamine H4 receptor.";  
RL Biochim. Biophys. Acta 1575:135-138(2002).  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).  
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
DR EMBL; AB053300; BAB83078.1; -.  
GO; GO:0016021; C:integral to membrane; IEA.

RESULT 6  
Q912Y3 PRELIMINARY; PRT; 389 AA.  
ID Q912Y3  
AC Q912Y3  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Histamine H4 receptor.  
OS Cavia porcellus (Guinea pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.  
OX NCBI\_TaxID=10141;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Liu C., Wilson S., Kuei C., Lovenberg T.W.;  
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).  
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
DR EMBL; AF358858; AAK97379.1; -.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0004872; F:receptor activity; IEA.  
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.  
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.  
DR Pfam; PF00001; 7tm\_1; 1.  
DR PRINTS; PR00237; GPCRHOOPSN.  
DR PRINTS; PR01726; HISTAMINEH4R.  
DR PROSITE; PS00237; G-PROTEIN RECEPT\_F1\_1; 1.  
DR PROSITE; PS0262; G-PROTEIN RECEPT\_F1\_2; 1.  
KW G-protein coupled receptor; Receptor; Transmembrane.

Query Match 34.1%; Score 698; DB 2; Length 445;  
Best Local Similarity 37.8%; Pred. No. 1.9e-43;

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EMBL; AF267537; AAF70947.1; --
EMBL; AF267538; AAF78950.1; --
InterPro; IPR000276; GPCR_Receptor.
DR Pfam; PF00001; 7tm_1_1; H3_receptor.
DR PRINTS; PR00237; GPCR_HODOPSIN.
DR PRINTS; PR01471; HISTAMINE_H3R.
DR PROSITE; PS00337; G_PROTEIN_RECEPTOR_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEPTOR_F1_2; 1.
KW Alternative splicing; G-protein coupled receptor; Glycoprotein;
Transmembrane.
FT DOMAIN 1 40 Extracellular (Potential).
FT TRANSMEM 41 61
FT DOMAIN 62 71 Cytoplasmic (Potential).
FT TRANSMEM 72 92
FT DOMAIN 93 109 Extracellular (Potential).
FT TRANSMEM 110 130
FT DOMAIN 131 157 Cytoplasmic (Potential).
FT TRANSMEM 158 178
FT DOMAIN 179 197 Extracellular (Potential).
FT TRANSMEM 198 218
FT DOMAIN 219 359 Cytoplasmic (Potential).
FT TRANSMEM 360 380
FT DOMAIN 381 398 Extracellular (Potential).
FT TRANSMEM 399 419
FT DOMAIN 420 445 Cytoplasmic (Potential).
FT TRANSMEM 446 465
FT DOMAIN 466 483 Poly-Ala.
FT CARBOHYD 11 11 N-linked (GlcNAc...) (Potential).
FT VARSPIC 276 305 Missing (in isoform Short).
FT SEQUENCE 445 AA; 48734 MW; BAE206A3887189A0 CRC64;
Query Match 34.1%; Score 697.5; DB 1; Length 445;
Best Local Similarity 37.5%; Pred. No. 2.1e-43;
Matches 159; Conservative 54; Mismatches 132; Indels 79; Gaps 9;
QY 18 LAFLMSLAFAITGNVAVILAFVADNRHRSNFFFLNLALSDFFVGVISPLIPIPTL 77
DB 38 LAALMALLIVATVGLNVALVAFVADSSLRQTQNFLLNLALSDFLVGVFCIPLVYPYL 97
QY 78 F-NMPPGSGICMFLITDYLCTASVYSLVLSYDRYQSVNAVRYAQTGILKIVQM 136
DB 98 TORWTFGRGLKMLVVDVLLCTSSVFNILVLSYDRFLSVTRAVSRAQGGDTRAVRNM 157
QY 137 VAVWILAFVNGPMILASDMSK-----NSTNTECEPGEVTEWYIIATIFLEFLPVSL 191
DB 158 VLVWVLAFLLYGPAIL---SWEVLSGGSSIPGHCVAEEFYNYWFLITASTLEFFTPFLS 214
QY 192 VYFVSQIY-----WSLWKGKGSLSRCPSS 214
DB 215 VTFFNLSIYNTQRTLRLLDGGAREAGDPLPEAQSSPPQPPGCGWCPKGGESMPL 274
QY 215 HAGFTATSRG--TGHSRRTGLACRTSLPGLKEPAASLHSESPRGKSSLLVLRTHMSG 272
DB 275 HRYGVGEAGPGAGEAALGGSGAAASTSSSGSSSRGTERPR----- 318
QY 273 IIAPKVGSFCRSESPVLHOR-----EHVELLRGRKLARSLLVLSAFAICWAPYCL 323
DB 319 --SLKGGKPSASSASLEKRMQVSGSITQRFRLSRDKKVAKSLAIVISIFGLCWAPYTL 376
QY 324 FTIVLSTVRGRPKSIWYSLAFWLOWFNSLNPFLYPLCHRRPQKAFKWLICVTK---Q 380
DB 377 LMIIRAAAC-HGHCVPDYPWYETSFLLWMANSVNPVLYPLCHYSFRAPFKLLCPQKLKQV 435
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QY 381 PAPS 384
DB 436 PHSS 439
RESULT 9
ID HH3R_HUMAN STANDARD; PRT; 445 AA.
AC Q9Y5N1; Q9GZX2; Q9HAK8;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE Histamine H3 receptor (HH3R) (G protein-coupled receptor 97).
DE 25-OCT-2004 (Rel. 45, Last annotation update)
GN Name=HRH3; Synonyms=GPCR97;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI TaxID=9606;
RN [1]_
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Thalamus;
RX MEDLINE=99278519; PubMed=10347254;
RA Lovenberg T.W., Roland B.L., Wilson S.J., Jiang X., Pyati J.,
RA Huvar A., Jackson M.R., Erlander M.G.;
RT "Cloning and functional expression of the human histamine H3
RT receptor.";
RL Mol. Pharmacol. 55:1101-1107(1999).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 2), AND CHARACTERIZATION.
RX MEDLINE=20568725; PubMed=11118334; DOI=10.1006/bbrc.2000.4008;
RA Nakamura T., Itadani H., Hidaka Y., Ohta M., Tanaka K.;
RT "Molecular cloning and characterization of a new human histamine
RT receptor, HH4R.";
RL Biochem. Biophys. Res. Commun. 279:615-620(2000).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORMS 1; 3; 4; 5; 6 AND 7).
RC TISSUE=Thalamus;
RX MEDLINE=21181559; PubMed=11284713; DOI=10.1042/0264-6021.3550279;
RA Coge F., Guenin S.-P., Audinot V., Renouard-Try A., Beauverger P.,
RA Maca C., Ouyry C., Nagel N., Rique H., Boutin J.A., Galizzi J.-P.;
RT "Genomic organization and characterization of splice variants of the
RT human histamine H3 receptor.";
RL Biochem. J. 355:279-288(2001).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANT SHY-DRAGER SYNDROME
RP VAL-280.
RC TISSUE=Blood;
RX MEDLINE=21953383; PubMed=11956964; DOI=10.1007/s007020200036;
RA Wiedemann P., Boenisch H., Oerters F., Brues M.;
RT "Structure of the human histamine H3 receptor gene (HRH3) and
RT identification of naturally occurring variations.";
RL J. Neural Transm. 109:443-453(2002).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM 3).
RA Ullmer C., Zirwes E., Lubbert H.;
RT "Cloning and functional expression of the human histamine H3
RT receptor.";
RL Submitted (MAR-2001) to the EMBL/GenBank/DBSJ databases.
RN [6]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=21638749; PubMed=11780052; DOI=10.1038/414865a;
RA Deloukas P., Matthews L.H., Ashurat J.L., Burton J., Gilbert J.G.R.,
RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA Beakley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
RA Chapman J.C., Clamp M., Collier R.E., Clark L.N., Clark S.Y., Clee C.M.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Coulson A., Coville G.J., Deadman R., Dhani P.D., Dunn M.,
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Graham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
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RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,  
RA Leivasalho M.H., Leversha M.A., Lloyd D., Lloyd D.M., Lovell J.D.,  
RA Marsh V.L., Martin S.L., McConachie L.J., McLaughlin K., McMurray A.A.,  
RA Milne S.A., Mistry D., Moore R.J.F., Mullikin J.C., Nickerson T.,  
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,  
RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,  
RA Rice C.M., Rose M.T., Scott C.E., Sehra H.K., Showkeen R., Sims S.,  
RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,  
RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,  
RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,  
RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,  
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,  
RA Rogers J.,  
RT "The DNA sequence and comparative analysis of human chromosome 20.",  
RL Nature 414:865-871(2001).  
CC -!- FUNCTION: The H3 subclass of histamine receptors could mediate the  
CC histamine signals in CNS and peripheral nervous system. Signals  
CC through the inhibition of adenylate cyclase and displays high  
CC constitutive activity (spontaneous activity in the absence of  
CC agonist). Agonist stimulation of isoform 3 neither modified  
CC adenylylate cyclase activity nor induced intracellular calcium  
CC mobilization.  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -!- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=7;  
CC Comment=Additional isoforms seem to exist;  
CC Name=1;  
CC IsoId=Q9Y5N1-1; Sequence=Displayed;  
CC Name=2;  
CC IsoId=Q9Y5N1-2; Sequence=VSP\_001886;  
CC Name=3; Synonyms=H3S;  
CC IsoId=Q9Y5N1-3; Sequence=VSP\_001885;  
CC Name=4;  
CC IsoId=Q9Y5N1-4; Sequence=VSP\_001881;  
CC Name=5;  
CC IsoId=Q9Y5N1-5; Sequence=VSP\_001882;  
CC Name=6;  
CC IsoId=Q9Y5N1-6; Sequence=VSP\_001883;  
CC Name=7;  
CC IsoId=Q9Y5N1-7; Sequence=VSP\_001884;  
CC -!- TISSUE SPECIFICITY: Expressed predominantly in the CNS, with the  
CC greatest expression in the thalamus and caudate nucleus. The  
CC various isoforms are mainly coexpressed in brain, but their  
CC relative expression level varies in a region-specific manner.  
CC Isoforms 3 and 7 are highly expressed in the thalamus, caudate  
CC nucleus and cerebellum while isoforms 5 and 6 show a poor  
CC expression. Isoforms 5 and 6 show a high expression in the  
CC amygdala, substantia nigra, cerebral cortex and hypothalamus.  
CC Isoform 7 is not found in hypothalamus or substantia nigra.  
CC -!- DISEASE: Defects in HRH3 are a cause of Shy-Drager syndrome  
CC [MIM:146500]. This syndrome is characterized by orthostatic  
CC hypotension, bladder and bowel incontinence, anhidrosis, iris  
CC atrophy, amyotrophy, ataxia, rigidity and tremor.  
CC -!- MISCELLANEOUS: Does not bind to cimetidine and triprolidine. Shows  
CC modest affinity for thioripamide, imetit, N-alpha-methylhistamine  
CC and R(-)-alpha-methylhistamine. Isoform 4 is unable to bind to  
CC iodoxyfentanyl while isoforms 1 and 3 bind it with high affinity.  
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.  
CC -----  
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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CC use by non-profit institutions as long as its content is in no way  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; AF140538; AAD38151.1; -;  
DR EMBL; AB045369; BAB20090.1; -;  
DR EMBL; AB019000; BAB17030.1; -;  
DR EMBL; AJ296652; CAC51025.1; -;  
DR EMBL; AJ278250; CAC39434.1; -;  
DR EMBL; AL078633; CAC04014.1; -;

DR EMBL; AF363791; AAKS0040.1; -;  
DR Genew; HGNC:5184; HRH3.  
DR MIM; 604525; -;  
DR MIM; 146500; -;  
DR GO; GO:0005887; C:integral to plasma membrane; TAS.  
DR GO; GO:0004969; P:histamine receptor activity; TAS.  
DR GO; GO:0007187; P:G-protein signaling, coupled to cyclic nucl.; TAS.  
DR GO; GO:0007269; P:neurotransmitter secretion; TAS.  
DR InterPro; IPR000276; GPCR\_Rhodopsin.  
DR InterPro; IPR003980; H3\_receptor.  
DR Pfam; PF00001; 7tm 1; 1.  
DR PRINTS; PR00237; GPCR\_RHODOPSIN.  
DR PRINTS; PR01471; HISTAMINEH3.  
DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
DR PROSITE; PS02662; G\_PROTEIN\_RECEP\_F1\_2; 1.  
KW Alternative splicing; Disease mutation; G-protein coupled receptor;  
KW Glycoprotein; Transmembrane.  
FT DOMAIN 1 39  
FT TRANSMEM 40 60  
FT DOMAIN 61 70  
FT TRANSMEM 71 91  
FT DOMAIN 92 108  
FT TRANSMEM 109 129  
FT DOMAIN 130 156  
FT TRANSMEM 157 177  
FT DOMAIN 178 196  
FT TRANSMEM 197 217  
FT DOMAIN 218 359  
FT TRANSMEM 360 380  
FT DOMAIN 381 395  
FT TRANSMEM 396 416  
FT DOMAIN 417 445  
FT DOMAIN 20 23  
FT DOMAIN 250 256  
FT DOMAIN 292 298  
FT CARBOHYD 11 11  
FT VARSPPLIC 85 98  
FT VARSPPLIC 197 315  
FT VARSPPLIC 227 342  
FT VARSPPLIC 234 263  
FT VARSPPLIC 274 353  
FT VARSPPLIC 445 445  
FT VARIANT 280 280  
FT CONFLICT 19 19  
FT SEQUENCE 445 AA; 48671 NW; 2ACF7440FBE95B6C CRC64;  
Query Match 33.9%; Score 693; DB 1; Length 445;  
Best Local Similarity 37.6%; Pred. No. 4.5e-43;  
Matches 163; Conservative 50; Mismatches 124; Indels 96; Gaps 11;

QY 18 LAFLSLAFAITIGNAVVILAFVADNRHRSNYPFLNLAIISDFVGVISIPLYIPHTL 77  
DB 37 LAALMALLIVATVIGNALVMAFVADSSLRNTQNNFLLNLAIISDFLVGFCLPYVYVL 96  
QY 78 F-NNPFGSGICMFILITDYLLTASVYSIVLSIDRYQSVSNARYRAQHTGLKIVAQM 136  
DB 97 TGRWTFGRGLCKLWLVDVYLLCTSSAFNLIVLSIDRFSLSVTRAVSVRAQQDTRRAVRKM 156  
QY 137 VAVWILAFVINGPMILASDSWK-----NSTNTECEPGFVTEWYILAITAFLEFLPVSL 191  
DB 157 LLVWVLAFLLYGFAIL---SWEYLSGGSGIPEGHCHYAEFFYNWYFLITASTLEFFTFPLS 213  
QY 192 VVYFVSQIY-----WSLWKRGSLSRCPGH 215  
DB 214 VTFFNLISLYNTRTRRLDGCAREAGPEPPPEAQPSPPPPPGCGCQKQGHGEAMPLH 273



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QY 216 -----AGFIATSSRGTHSRRTGLACRTSLPGLKEPAASLHSESPRGKSSLLV 263
DB 274 RYGVCEAAVGAEGATLGGGGGGS-----VASPTSSSG-----SSRGTERPR----- 318
QY 264 SLRTHMSGSIIFKVGSCRESPLVHOR-----EHVELLRGRKLARSLAVLLSAP 314
DB 319 -----SLKRGSKPSASSASLEKRMKMWVSQSFTQRFRLSRDRKVAKSLAVIVSIF 367
QY 315 AICWAPYCLFIVTLSTYRGRPKSIWYSIAFWLQWPNLSLNPFLYPLCHRRFPQAFWKI 374
DB 368 GLCWAPYTLIIIRAAAC-HGHCVPDYWYETSFLLWANSVNPVLPYLCHHSFRFAFTKL 426
QY 375 LCVTK---QPAPS 384
DB 427 LCPQKLKIOPHSS 439

RESULT 10
HH3R_MOUSE
ID HH3R_MOUSE STANDARD; PRT; 445 AA.
AC P58406;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Histamine H3 receptor (HH3R).
GN Name=Hrh3;
OS Mus musculus (Mouse);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CD-1;
RA Coge P., Rique H., Levacher B., Leopold O., Guenin S.-P., Boutin J.A.,
RA Galizzi J.-P.;
RT Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: The H3 subclases of histamine receptors could mediate the
CC histamine signals in CNS and peripheral nervous system. Signals
CC through the inhibition of adenylyate cyclase and displays high
CC constitutive activity (spontaneous activity in the absence of
CC agonist) (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC
CC EMBL; AY044153; AAK72406.1; -.
CC MGD; MGI:2139279; Hrh3.
CC DR InterPro; IPR000276; GPCR Rhodopsin.
CC DR InterPro; IPR003980; H3_receptor.
CC DR Pfam; PF00001; 7cm1; 1.
CC DR PRINTS; PR00237; GPCRHHODOPSIN.
CC DR PRINTS; PR01471; HISTAMINEH3R.
CC DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
CC DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_2; 1.
CC DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Glycoprotein; Transmembrane.
FT DOMAIN 1 39 Extracellular (Potential).
FT TRANSMEM 40 60 Potential.
FT DOMAIN 61 70 Cytoplasmic (Potential).
FT TRANSMEM 71 91 Potential.
FT DOMAIN 92 108 Extracellular (Potential).
FT TRANSMEM 109 129 Potential.
FT TRANSMEM 130 156 Cytoplasmic (Potential).
FT TRANSMEM 157 177 Potential.
FT DOMAIN 178 196 Extracellular (Potential).
FT TRANSMEM 197 217 Potential.
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FT DOMAIN 218 359 Cytoplasmic (Potential).
FT TRANSMEM 360 380 Potential.
FT DOMAIN 381 396 Extracellular (Potential).
FT TRANSMEM 397 417 Potential.
FT DOMAIN 418 445 Cytoplasmic (Potential).
FT DOMAIN 20 23 Poly-Ala.
FT CARBOHYD 11 11 N-linked (GLCNAC..) (Potential).
SQ SEQUENCE 445 AA; 48541 MW; B8D406E29E1F3C5F CRC64;

Query Match 33.5%; Score 686; DB 1; Length 445;
Best Local Similarity 37.1%; Pred. NO. 1.5e-42;
Matches 159; Conservative 49; Mismatches 140; Indels 80; Gaps 10;

QY 18 LAFLMSLLAFATIGNAVVILAFVADRLNRHSVFLNLAIISDFVGVISILPLYIPHTL 77
DB 37 LAALMALIVATVIGNALVULAFVADSLRQTQNNFFLLNLAIISDFVGVISILPLYIPHTL 96
QY 78 F-NMNPSSGICMFWLITDYLCTASVYSIVLISYDRYQSVSNVAVRYRAQHTGILKIVAQM 136
DB 97 TGRWTFGRGLCKLWLVVDYLLCASSVFNILISYDRPLSVTRAVSYRAQOGDTRRAVRKM 156
QY 137 VAVWILAFVNGPMILASDSWK-----NSTWTECEPGFVTEWYILAITAFLEPLPVSL 191
DB 157 ALWVLAFLLYGPAIL-----SWEYLSGGSSIDEGHCYAEFFYNWYFLITASTLEFFTPFLS 213
QY 192 VYFVSQIY-----WSLWKRGLSRCPSH 215
DB 214 VTFNLSIYLNIOQRTRLRDGREGPEPPDQAQPPPPPPGKCGKPGHGMPLH 273
QY 216 -----AG-FIATSSRGTHSRRTGLACR-----TSLPGLKEPAASLHSESPRGKSSLL 262
DB 274 RYGVCEAGPGVETGEAGLGGGGGGAASPTSSSSSSSRGTERPRSLKRGSKPSASSASL 333
QY 263 VSLRTHMSGSIIFKVGSCRESPLVHORHVELLRGRKLARSLAVLLSAPFAICWAPYC 322
DB 334 EKRMMVQSQT-----TQRFRLSRDKKVAKSLAIIIVSIFGLCWAPYT 375
QY 323 LFTIVLSTYRGERPKSIWYSIAFWLQWPNLSLNPFLYPLCHRRFPQAFWKILCVTK--- 379
DB 376 LLMIRAAAC-HGHCVPDYWYETSFLLWANSVNPVLPCHYSFRRAFTKLCPQKLKV 434
QY 380 QPAPSQTQ 387
DB 435 QPHGSLEQ 442
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## RESULT 11

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HH3R_MOUSE
ID HH3R_MOUSE STANDARD; PRT; 445 AA.
AC Q9QYN8; Q9QYN6; Q9QYN7; Q9QYN9;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Histamine H3 receptor (HH3R).
GN Name=Hrh3;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Hypothalamus;
RC MEDLINE=20330707; PubMed=10869375;
RA Lovenberg T.W., Pyati J., Chang H., Wilson S.J., Erlander M.G.;
RT "Cloning of rat histamine H3 receptor reveals distinct species
RT pharmacological profiles.";
RL J. Pharmacol. Exp. Ther. 293:771-778 (2000).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC TISSUE=Striatum;
RX MEDLINE=21016732; PubMed=11130725; DOI=10.1038/35048583;
RA Morisset S., Rouleau A., Ligneau X., Gbahou F., Tardivel-Lacombe J.,
RA Stark H., Schunack W., Ganelin C.R., Schwartz J.-C., Arrang J.-M.;
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RN RP SEQUENCE FROM N.A.
RA Tracey A.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
DR EMBL; AL928906; CAE49238.1; -.
DR ZFIN; ZDB-GENE-040724-204; si:rp71-34g2.4.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:histamine receptor activity; IEA.
DR GO; GO:0004969; F:histamine receptor activity; IEA.
DR GO; GO:0001584; P:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor activity; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsin.
DR InterPro; IPR003980; H3_receptor.
DR Pfam; PF00001; 7cm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPSIN.
DR PRINTS; PR01471; HISTAMINEH3R.
DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECP_F1_2; 1.
DR PROSITE; PS0262; G_PROTEIN_RECP_F2_1; 1.
DR G-protein coupled receptor; Receptor; Transmembrane.
KW G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 473 AA; 53506 MW; 032FC7C27D8C6E57 CRC64;

Query Match 32.8%; Score 671; DB 2; Length 473;
Best Local Similarity 38.1%; Pred. No. 2e-41;
Matches 169; Conservative 60; Mismatches 143; Indels 72; Gaps 15;

QY 1 MSEGNDVLP-----TAQVPLFLMSLLAFATIGNAVVILAFVADRN 45
DB 35 MERENATSLADLTFFENRAQYGFSPSTSLFTVLTMLLVPAIVLGNALVILAFVWEKS 94
QY 46 LRHSNYPFLNATSDFPVGVISPLYPHTLP-NWNPSSGICMFLITDYLCTASVYS 104
DB 95 LRTQGNFFFLNALADFLVGGFCIPVLYVTGEWRLGRGCKLWLVVDMLCTASVFN 154
QY 105 IVLISYDRYQSVNAVRYRAQHTGLK-IVAQMVAWVILAEVLNPGMILASDSKNSNT 163
DB 155 IVLISDFRQSVTKAVSYRCQ-KGITKDAVLKMLCVLAAFLYGPAIL---SWEHTGG 210
QY 164 E-----ECEPFTVEWYILATAFLEFLPLVSLVYPSVQIYWSLWKR----- 206
DB 211 SVVPDGECAEFYFNWYFLMTASTVEFTPTFTISVFNLSIYINRNCAMREEOPTYVR 270
QY 207 -GSLRCPSHAG-----FIATSRGTGHSRTGLACRTSLPGL-----KEPAASLHS--E 253
DB 271 LRSFKMKPLGADVQVRFV----RPVESRVADLASRCCRLASTAKVSAAEFGNGRQ 326
QY 254 SPRGKSSLLVSLRTHMSGSIIAFKVGSF---CRSESPVLHQEHV-----ELLRGRKL 303
DB 327 SKRRDSTLADLPPLQVEERILAASEAQPHYVDHSAGPHRRPDMVASLANRFLSRDKKV 386
QY 304 ARSLAVLLSAFAICWAPYCLFTIVLSTYRRGERPKSIWYSIAFWLQWNSLNPFLYPLC 363
DB 387 AKSLAVIVCVFGLCWAPYTLMIIRAAC-HGQCQVQHYLYEISFWLLWINSINPILYPLC 445
QY 364 HRRFOKAFWKILCVTKQAPSQO 387
DB 446 HSRFKRAFSKLLC-----PSKTK 463
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RESULT 13
Q8WY01 PRELIMINARY; PRT; 365 AA.
AC Q8WY01;
DT 01-MAR-2002 (TRENBLRel. 20, Created)
DT 01-MAR-2002 (TRENBLRel. 20, Last sequence update)
DT 01-MAR-2004 (TRENBLRel. 26, Last annotation update)
DE Histamine H3 receptor isoform 2.
GN Name=HRH3;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
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RN RP SEQUENCE FROM N.A.
RC TISSUE=Hippocampus;
RA Wellendorph P.; Goodman M.W., Burstein E.S., Nash N.R., Brann M.R.,
RA Weiner D.M.;
RT "Molecular Cloning and Characterization of Functionally Distinct
RT Isoforms of the Human Histamine H3 Receptor.";
RL Neuropharmacology 0:0-0(2002)
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
DR EMBL; AF321911; AAL71912.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004969; F:histamine receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; P:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor activity; IEA.
DR Pfam; PF00001; 7cm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPSIN.
DR PRINTS; PR01471; HISTAMINEH3R.
DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECP_F1_2; 1.
DR PROSITE; PS0262; G_PROTEIN_RECP_F2_1; 1.
DR G-protein coupled receptor; Receptor; Transmembrane.
KW G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 365 AA; 40609 MW; D78B32042464CB35 CRC64;

Query Match 32.2%; Score 658; DB 2; Length 365;
Best Local Similarity 39.0%; Pred. No. 1.4e-40;
Matches 152; Conservative 44; Mismatches 104; Indels 90; Gaps 11;

QY 18 LAFILMSLLAFATIGNAVVILAFVADRNLRHSNYPFLNATSDFPVGVISPLYPHTL 77
DB 37 LAALMALLIVATVLGNALVILAFVADSLRTQNNFFLNLALISDFLVGAFCLPLVYPVL 96
QY 78 P-NWNPSSGICMFLITDYLCTASVYSIVLISYDRYQSVNAVRYRAQHTGLKIVQM 136
DB 97 TGRWTFGRGLCKLWLVVDYLCTSAFNILVLSYDRFLSVTRAVSYRAQQGDTREAVRM 156
QY 137 VAVVILAEVLNPGMILASDSWK-----NSTNTECEPFTVEWYILATAFLEFLPLVSL 191
DB 157 LLVWVLAFLYGPAIL---SWEYLSGGSSIPEGHCYAEFFYNWYFLITASTLEFFTPLS 213
QY 192 VYFSVQIYWSLWKRGLSRCPSHAGFTATSSRTGHSRTGLACRTSLPGLKE----- 245
DB 214 VTFFNLISYLN-----QRRT-----RLLDGAREAAAGPEP 244
QY 246 -PAASLHSESPRGKSSLLVSLRTHMSGSIIAFKVGSF-----RSESPVLHQEHVEL 297
DB 245 PPEAQSPSPPPPG-----CWGCWQKHGGEAMPLH----- 273
QY 298 LRGRKLARSLAVLLSAFAICWAPYCLFTIVLSTYRRGERPKSIWYSIAFWLQWNSLNP 357
DB 274 --RKVAKSLAVIVSIFGLCWAPYTLMIIRAAC-HGCHVDYDWTSETSWLLMANSVNP 329
QY 358 FLYPLCHRRFPQAFWKILCVTK---QPAPS 384
DB 330 VLYPLCHHSFRRAFTKLLCPQLKIQPHSS 359

RESULT 14
Q8WXX29 PRELIMINARY; PRT; 373 AA.
AC Q8WXX29;
DT 01-MAR-2002 (TRENBLRel. 20, Created)
DT 01-MAR-2002 (TRENBLRel. 20, Last sequence update)
DT 01-MAR-2004 (TRENBLRel. 26, Last annotation update)
DE Histamine H3 receptor isoform 4.
GN Name=HRH3;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Hippocampus;
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